FIG.1

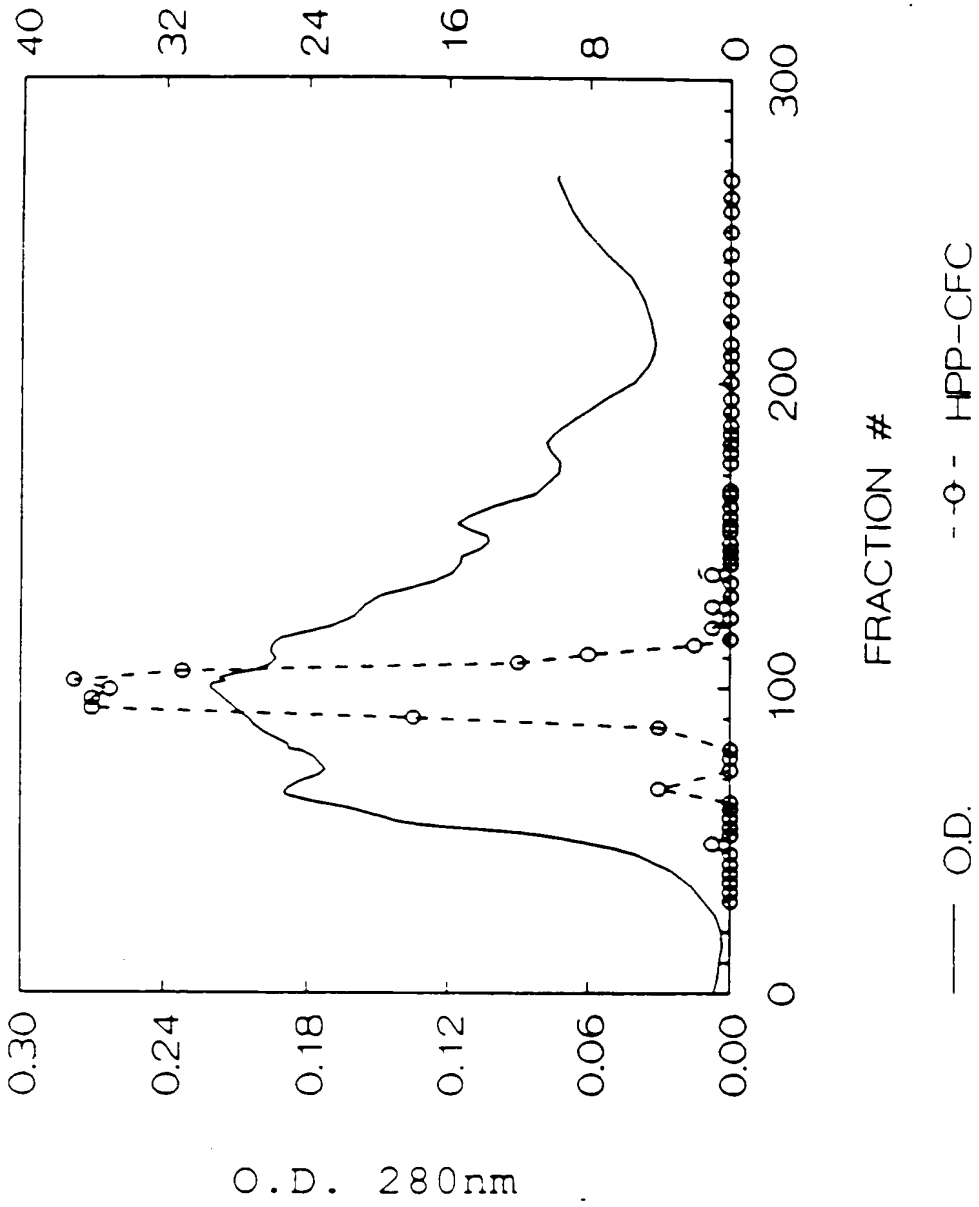

HPP-CFC (Colony #)
40
32
24
16
8
0
300
200
100
0
0.30
0.24
0.18
0.12
0.06
0.00
O.D. 280nm
FRACTION #
O.D.
HPP-CFC

FIG.2

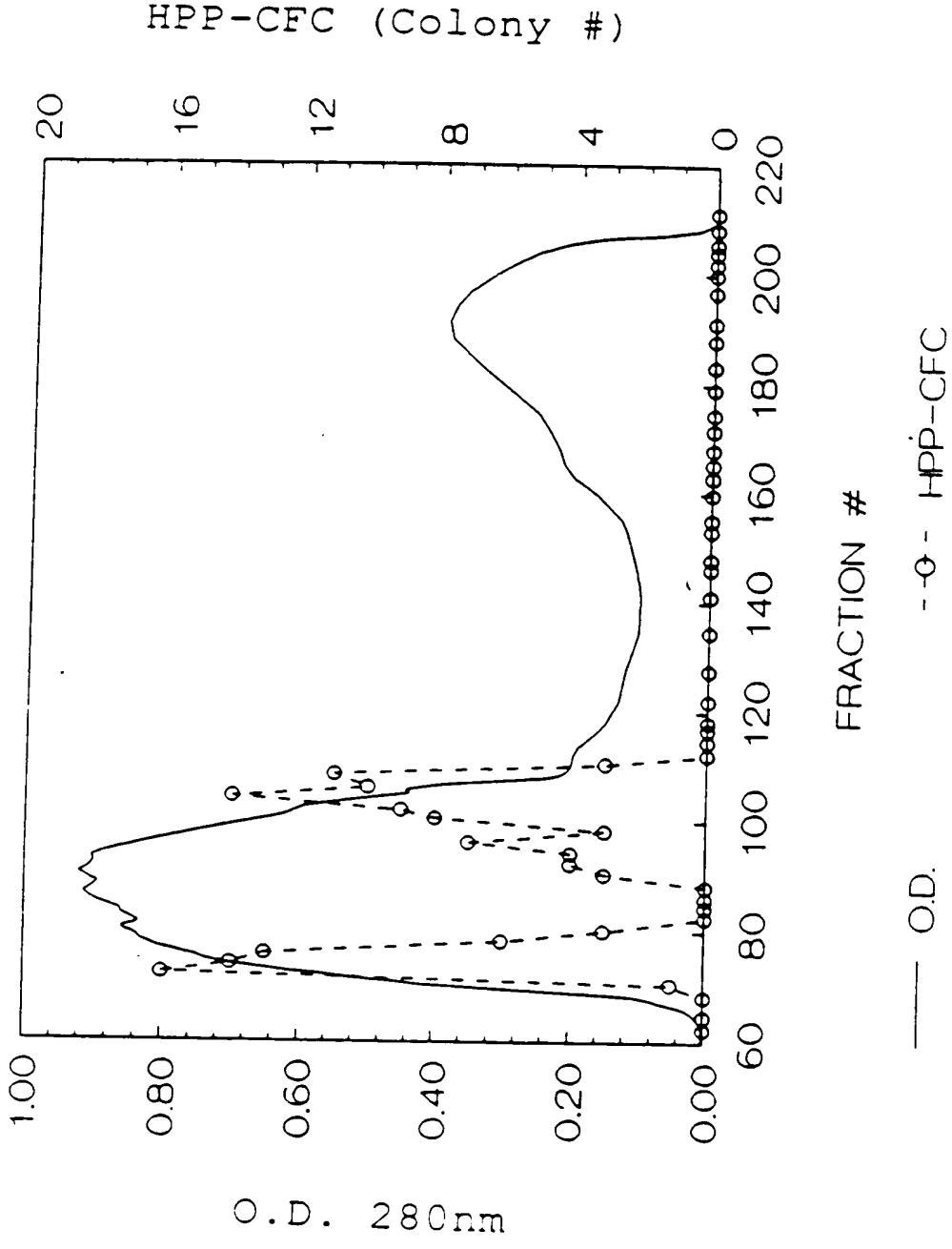

HPP-CFC (Colony #)
20
16
12
8
4
0
220
200
180
160
140
120
100
80
60
FRACTION #
- -o- - HPP-CFC
—— O.D.
1.00
0.80
0.60
0.40
0.20
0.00
O.D. 280nm

FIG.3

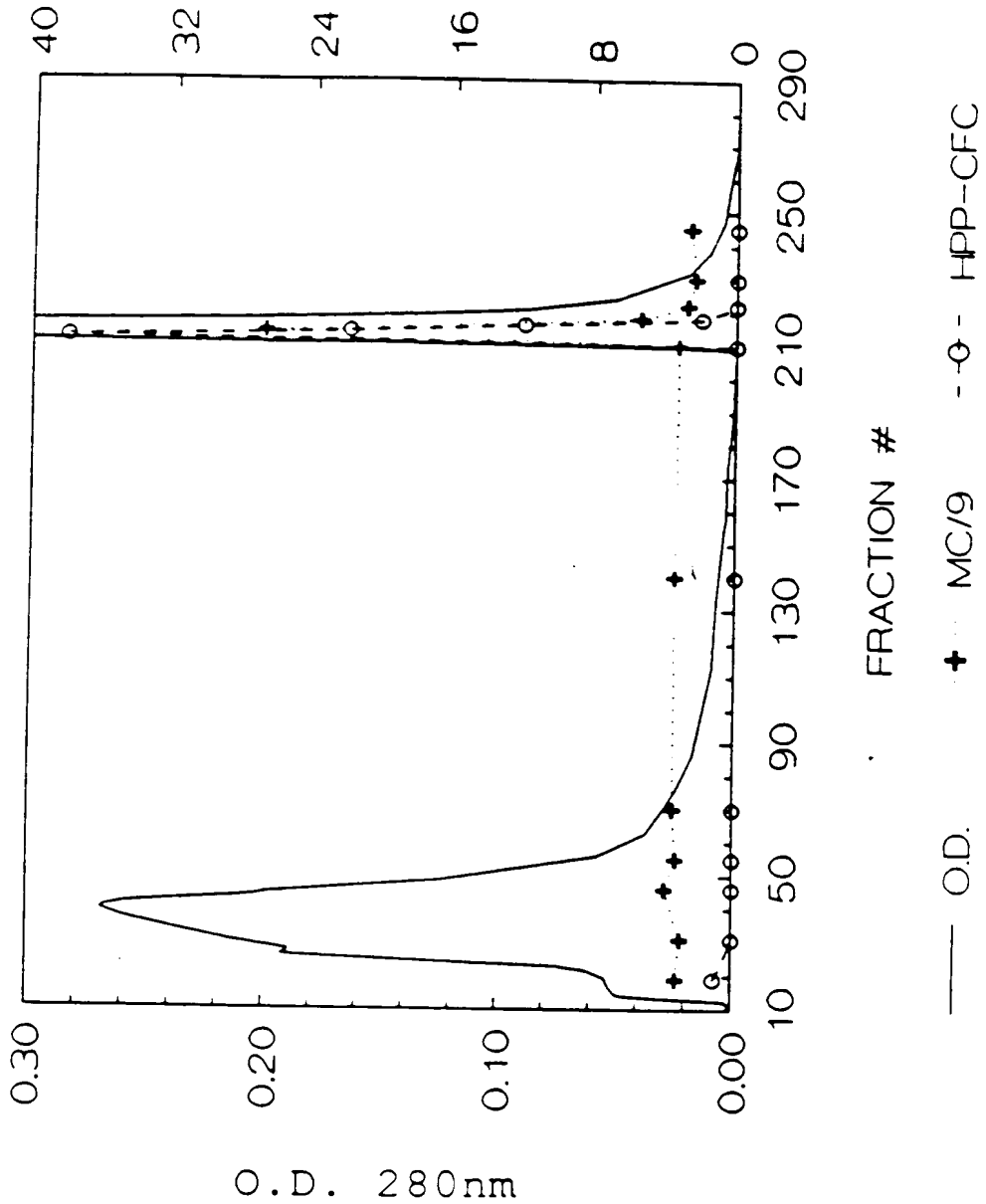

MC/9 CPM (X 10-3) or HPP-CFC (col. #)
40
32
24
16
8
0
290
250
210
170
130
90
50
10
FRACTION #
0.30
0.20
0.10
0.00
O.D. 280nm
O.D.
MC/9
HPP-CFC

FIG. 4

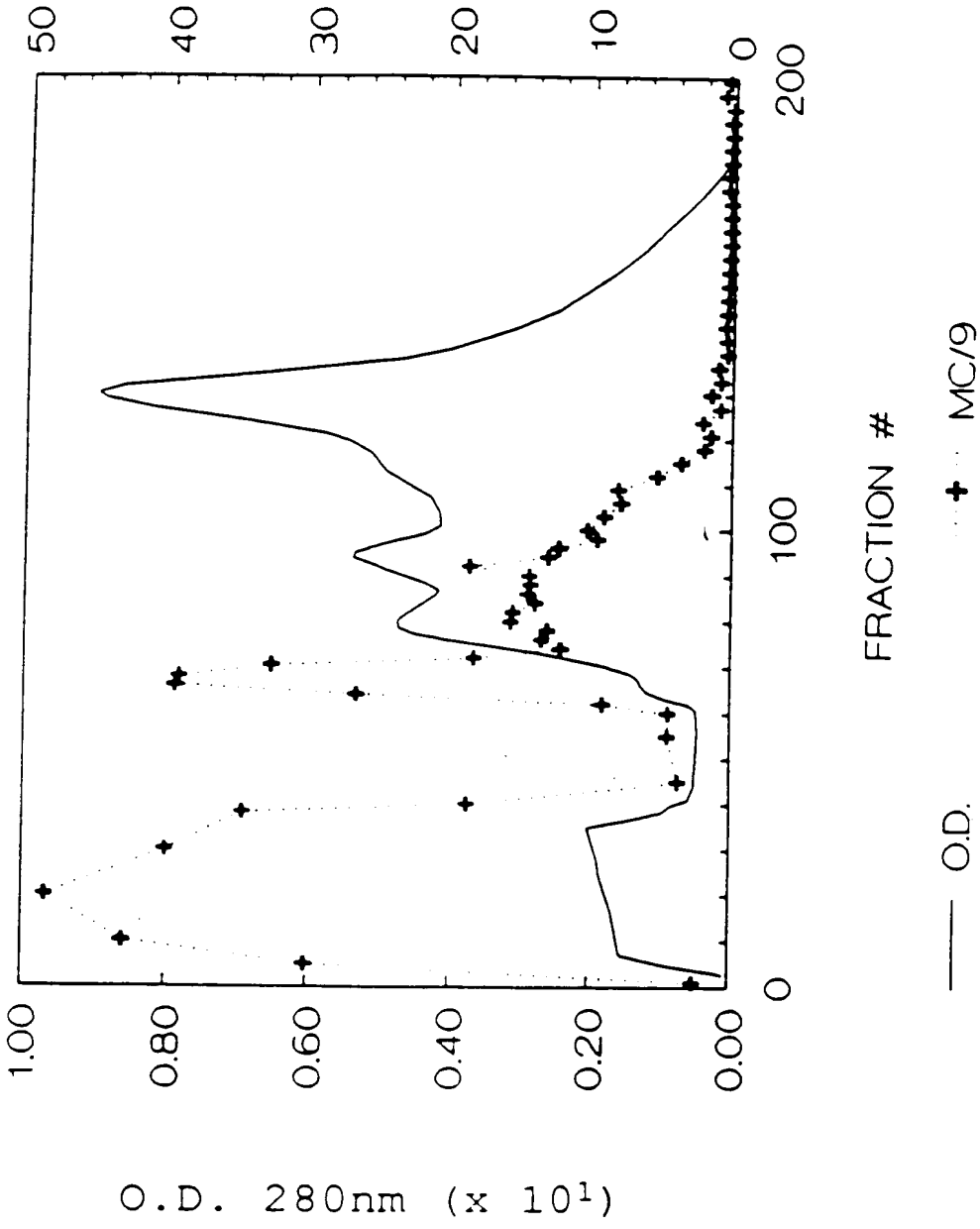

MC/9 CPM (x 10^{-3})
50
40
30
20
10
0
200
100
0
1.00
0.80
0.60
0.40
0.20
0.00
O.D. 280nm (x 10^{1})
FRACTION #
MC/9
O.D.

FIG.5

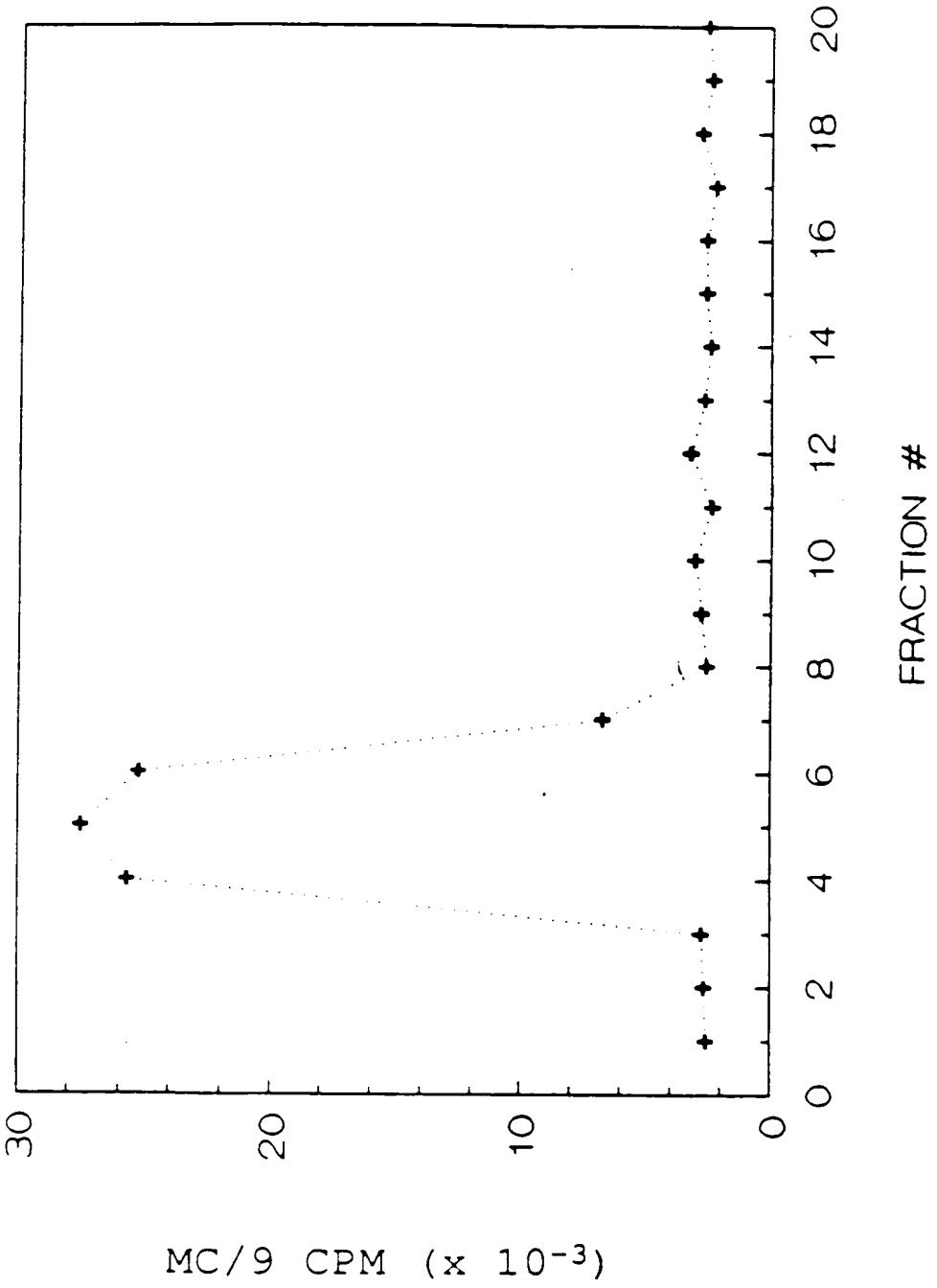


FIG. 6

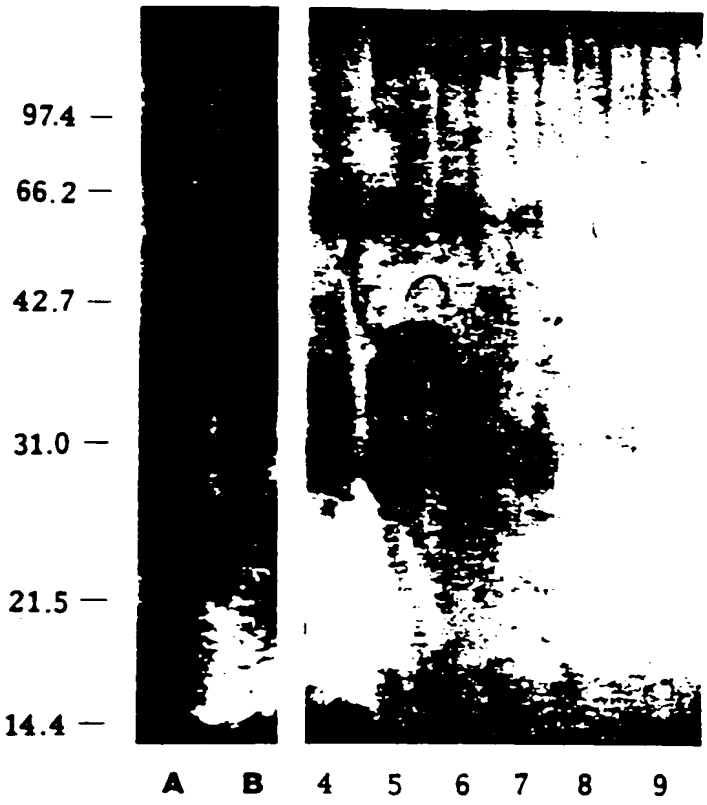


FIG.7

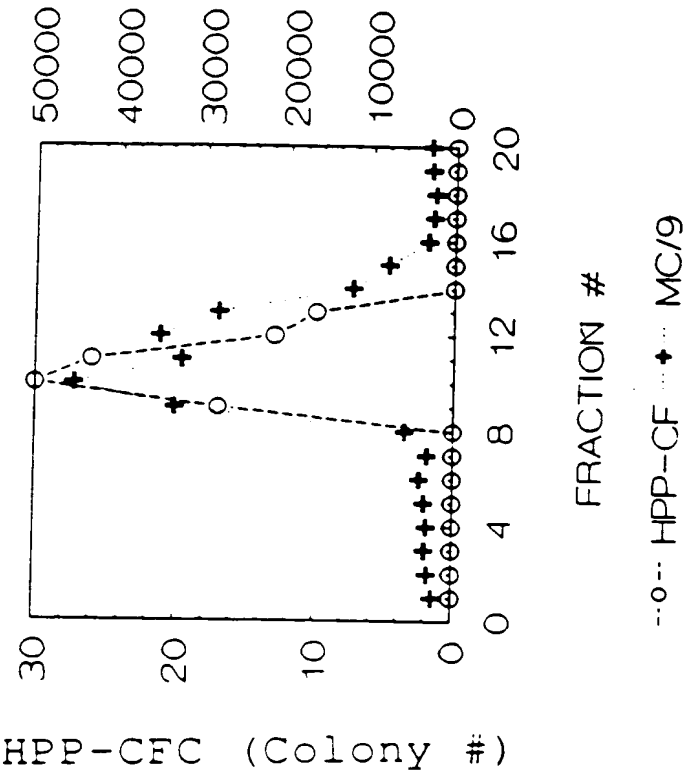

MC/9 CPM
50000
40000
30000
20000
10000
0
0
4
8
12
16
20
FRACTION #
--o-- HPP-CF + MC/9
30
20
10
0
HPP-CFC (Colony #)

FIG. 8

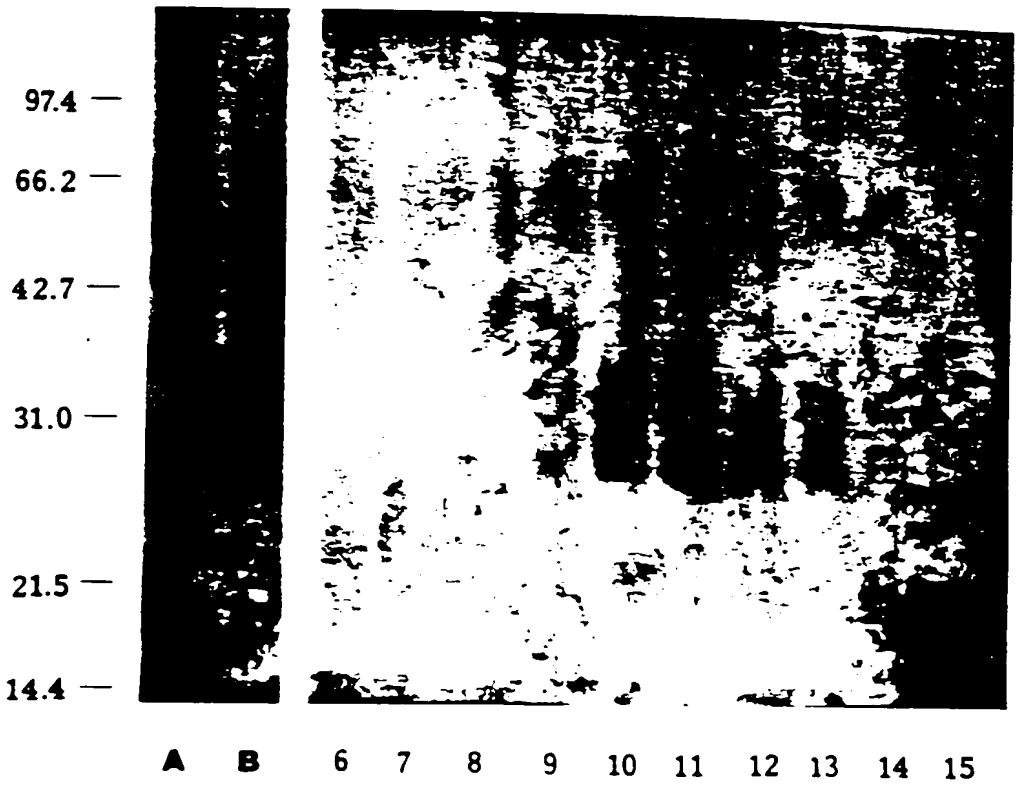


FIG.9

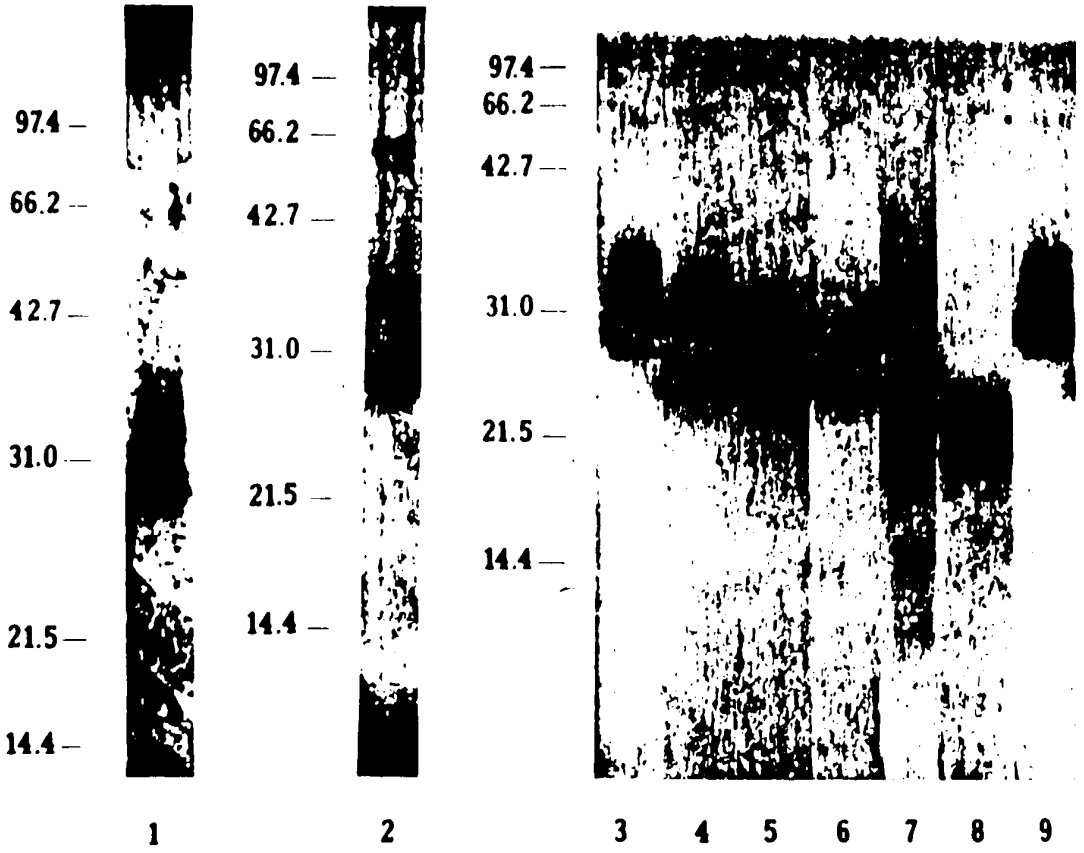

97.4
66.2
42.7
31.0
21.5
14.4
1
97.4
66.2
42.7
31.0
21.5
14.4
2
97.4
66.2
42.7
31.0
21.5
14.4
3
4
5
6
7
8
9

FIG.10

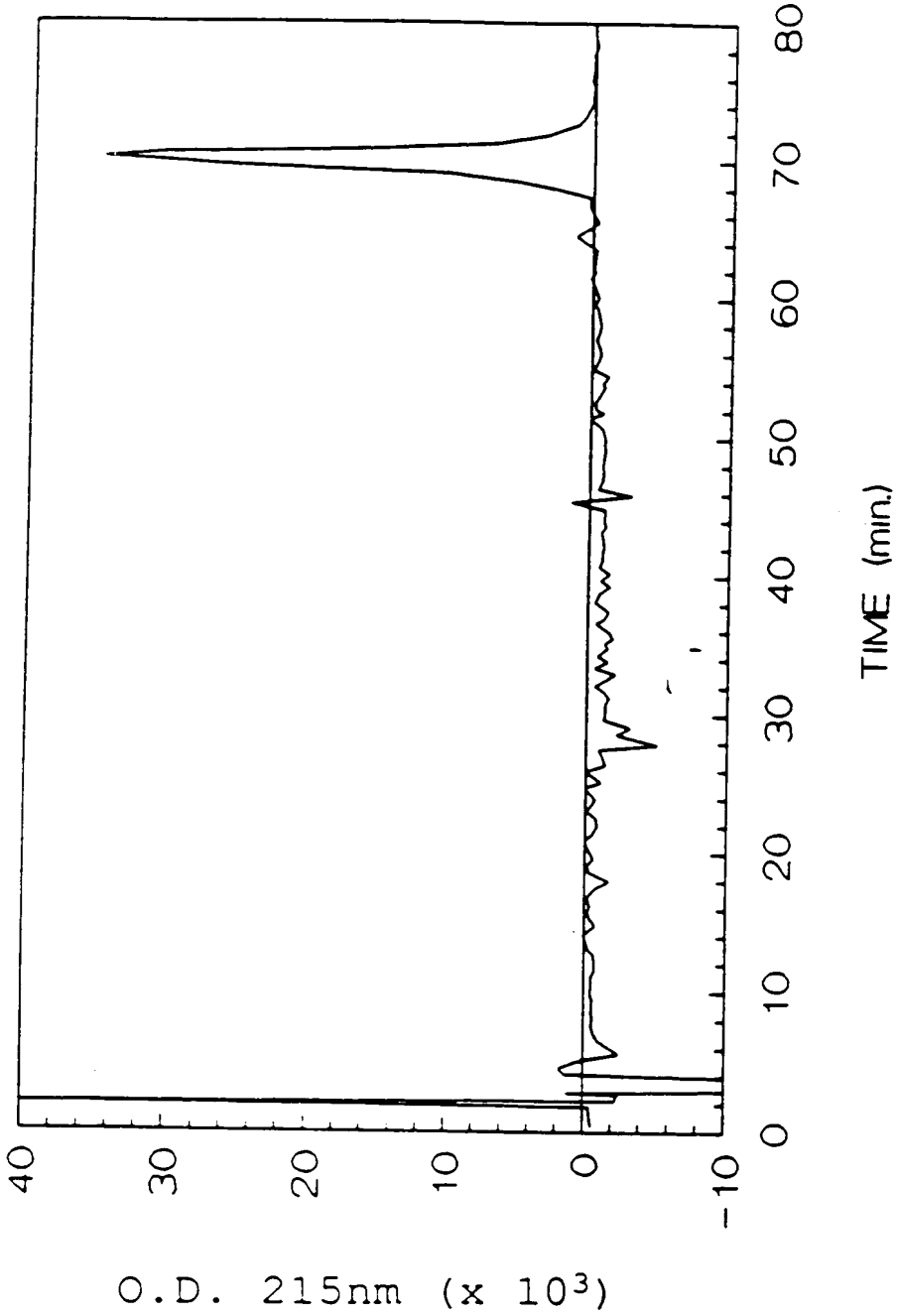


FIG.11

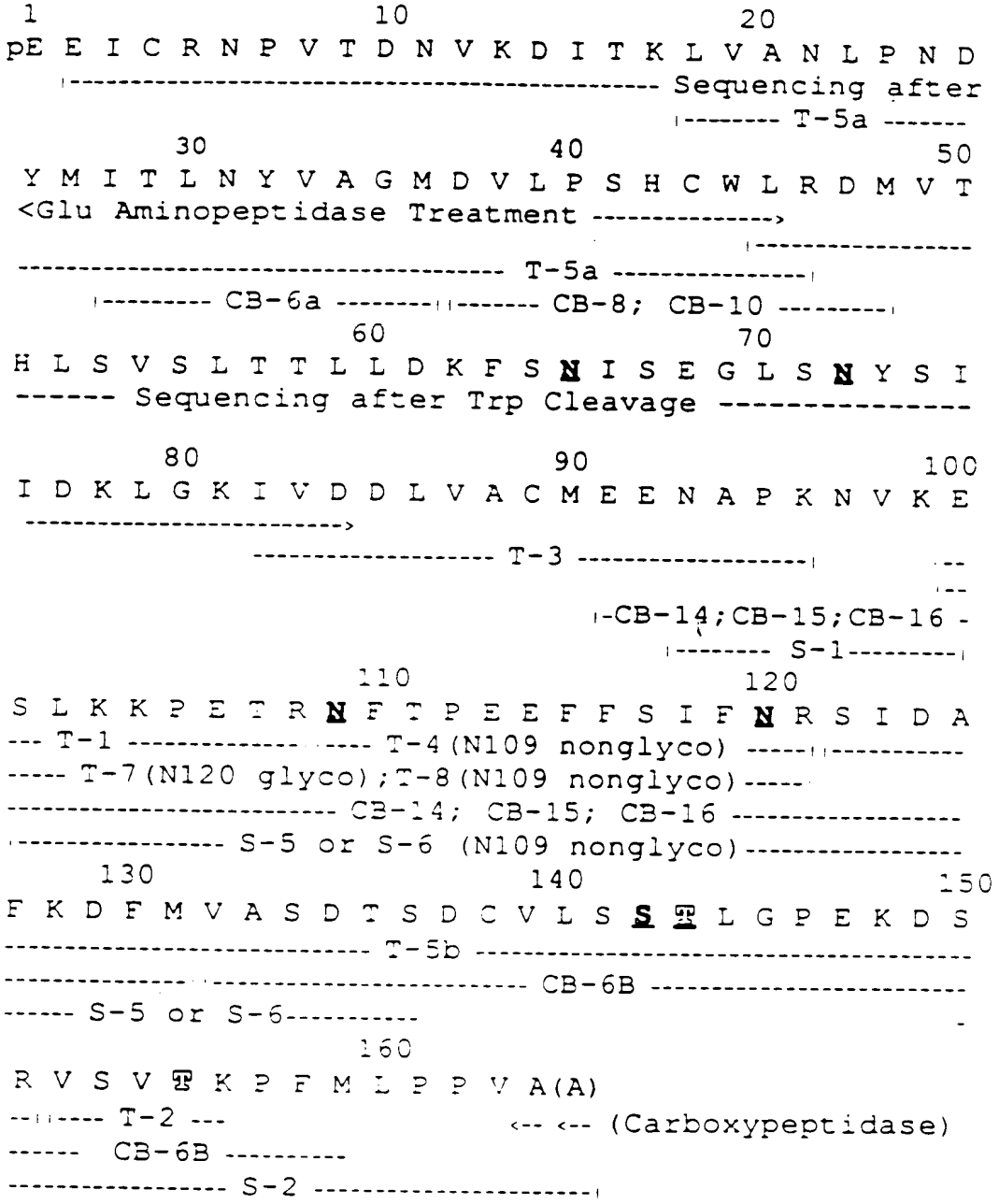

1 10 20
pE E I C R N P V T D N V K D I T K L V A N L P N D
Sequencing after
T-5a
30 40 50
Y M I T L N Y V A G M D V L P S H C W L R D M V T
<Glu Aminopeptidase Treatment
T-5a
CB-6a
CB-8; CB-10
60 70
H L S V S L T T L L D K F S N I S E G L S N Y S I
Sequencing after Trp Cleavage
80 90 100
I D K L G K I V D D L V A C M E E N A P K N V K E
T-3
CB-14;CB-15;CB-16
S-1
110 120
S L K K P E T R N F T P E E F F S I F N R S I D A
T-1
T-4(N109 nonglyco)
T-7(N120 glyco);T-8(N109 nonglyco)
CB-14; CB-15; CB-16
S-5 or S-6 (N109 nonglyco)
130 140 150
F K D F M V A S D T S D C V L S S T L G P E K D S
T-5b
CB-6B
S-5 or S-6
160
R V S V T K P F M L P P V A(A)
T-2
(Carboxypeptidase)
CB-6B
S-2

FIG.12A

OLIGO	SEQUENCE	LOCATION
219-21	ACATTCTTIGGIGCATTCTCCTCCAT G T G T T	393-368
219-22	AAAAACTCCTCIGGIGTAAAATT G T T G G	447-425
219-25	GTTTCNGGTTTTTT C C C	420-407
219-26	ATGGAAGAAAACGCCCCCAAAAACGT G G T G T	368-393
222-11	CCNAATGATTATATGATAAC C C C C T	167-186
222-12	GGNGGNAACATAAANGGCTT G G T	566-585
223-6	ACCATAAAATCTTTAAAICGATC G G C G G	492-470
224-24	GTATTTTCAATAGATCCATTGA	450-471
224-25	CCAACTATGTCGCC	190-202
224-27	GTAGTCAAGCTGACTGATAAG	273-253

FIG.12A CONT.'

224-28	TAACCAACAATGACTAGGCAA	235-215	
225-31	TTCCAGAGTCAGTGTC	547-562	
227-29	GCGAAGCTTGCCTTTCCTTATGAAGAAGA	16-35	*
227-30	GCGCCGCGGTTACGGTGGTAACATGAAGGGCTTTGTGA	586-561	*
228-30	GATAAATGCAAGTGATAATCC	45-65	
230-25	GCGGTCGACCCGCGGAACTTTAAGTCCATGCAACAC	705-685	*
237-19	CACCCGCGGTTATGCAACAGGGGGTAACATAAATGG	569-592	*
237-20	CACCCGCGGTTAGGCTGCAACAGGGGGTAACATAAA	572-595	*

FIG.12B

OLIGO	SEQUENCE	LOCATION
231-27	CTTAATGTTGAAGAAACC	703-686
233-13	GATGGTAGTACAATTGTCAGAC	410-431
233-14	GTCTGACAATTGTACTACCATC	431-410
235-29	CAATTTAGTGACGTCTTTTACA	302-323
235-30	TTAGATGAGTTTTCTTTCACGCAC	556-533
235-31	AAATCATTCAAGAGCCCAGAACCC	566-589
236-31	AACATCCATCCCGGGGAC	366-383
238-31	CTGGCAATATTTTAAGTCTCAAGAAGACC	
241-6	GCGCCGCGGCTCCTATAGGTGCTAATTGG	
254-9	CCTCACCACTGTTTGTGCTGGATCGCA	153-179
262-13	GGTGTCTAGACTTGTGTCTTCTTCATAAGGA	209-190

FIG.12C

OLIGO	SEQUENCE
201-7	CCCCCCCCGG T A
220-3	TTTTTTTTTTTTTTTTTGG
220-7	TTTTTTTTTTTTTTTTTAG
220-11	TTTTTTTTTTTTTTTTTCG
221-11	TTCGGCCGATCAGGCCCCCCCCC
221-12	TTCGGCCGGATAGGCCTTTTTTTTTTTTT
228-28	GGCCGGATAGGCCTCACNNNNNNT
228-29	GGCCGGATAGGCCTCAC

FIG.13A

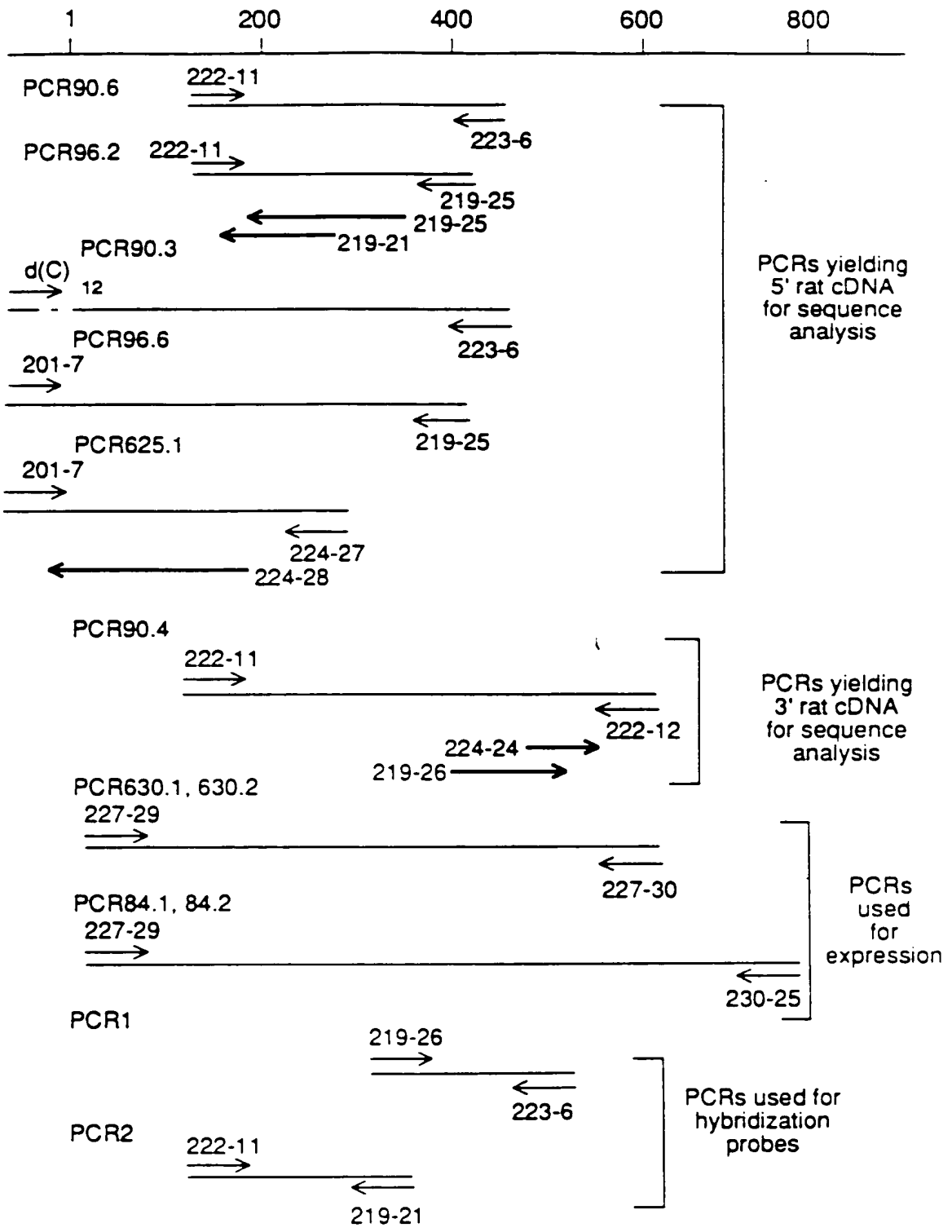

1
200
400
600
800
PCR90.6
222-11
223-6
PCR96.2
222-11
219-25
219-25
219-21
PCR90.3
d(C) 12
223-6
PCR96.6
201-7
219-25
PCR625.1
201-7
224-27
224-28
PCRs yielding 5' rat cDNA for sequence analysis
PCR90.4
222-11
222-12
224-24
219-26
PCRs yielding 3' rat cDNA for sequence analysis
PCR630.1, 630.2
227-29
227-30
PCR84.1, 84.2
227-29
230-25
PCRs used for expression
PCR1
219-26
223-6
PCR2
222-11
219-21
PCRs used for hybridization probes

FIG. 13B

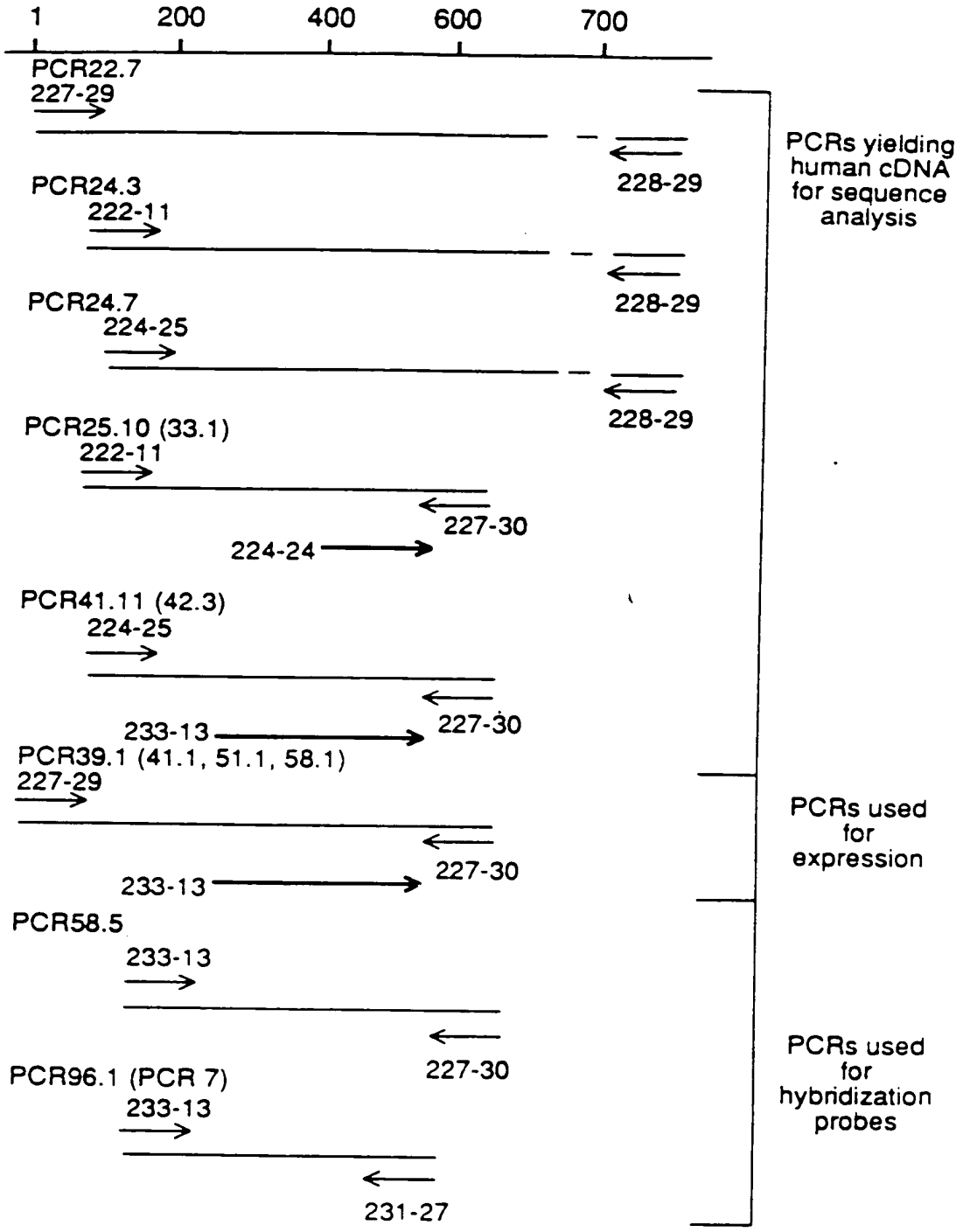

1
200
400
600
700
PCR22.7
227-29
228-29
PCR24.3
222-11
228-29
PCR24.7
224-25
228-29
PCR25.10 (33.1)
222-11
227-30
224-24
PCR41.11 (42.3)
224-25
227-30
233-13
PCR39.1 (41.1, 51.1, 58.1)
227-29
227-30
233-13
PCR58.5
233-13
227-30
PCR96.1 (PCR 7)
233-13
231-27
PCRs yielding human cDNA for sequence analysis
PCRs used for expression
PCRs used for hybridization probes

FIG.14A

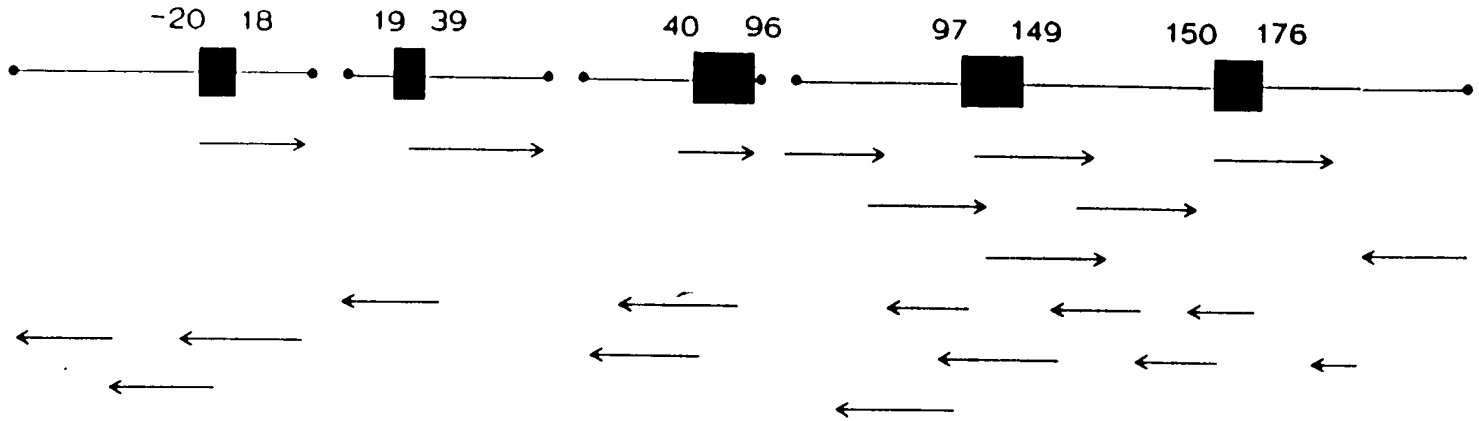


FIG.14B

```
AAAGTATCTTTCTATTGGCGAAGGACATGTTTTCCcATAAGTGGT    45

AAACAnACTGTCTGCACATAATAATTATCTTGCTGCCGTAAAGAT    90

TAGGTTAAATTCTGcCTTCGATCTAAAAACACACCCTTCTGTCAA   135

TCCGAGGAGCAGTGTGCTAGTCTAGAGGTCTAAATGAAGGCTCCT   180

TTCACGGTTGTATTTCTGCTCCCCAAATTGTCCACATTTAAAAGG   225

AGAGTGCTTCTTTTCAGCCTTAGGCTCTGAATTTCATGCATTCCT   270

CCATTTTCCGAGGTCCCccCcAAGTGATAATTCTGTTACACGTTG   315

CTACAAGTTCATCCCTAATTGCCGTCAAGAAACTGACTGTAGAAG   360

GCTTACCACAGACGTTGTAACCGACAGTAAAGCCATTGAAAGAGT   405

AATTCAAACAGGATGGAAGCCAGGAGTATTTTGTGGCTGTTGCTC   450

TTTTTCTTTTCAGTTTGGTGAGAGCAGCTTGAATGCTTAACATTT   495

AAGCCATCAGCTTAAAACAAAACAAAACAAAACAAAAAAAAACCC   540

CGCTCTGGCATATTTGCACTTAACACATACGGTATAAGGTGTTAC   585

TGGTTTGCATAGTTCTGGATTTTTTTTTTTTAAAAACTGATGGAC   630

                                    -20
                                    ThrTrpIleIleThrC
ACCAAGAAATGTTTCTGTTCTTTGTTTAGACTTGGATTATCACTT   675

                  -10
ysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrG
GCATTTATCTTCAACTGCTCCTATTTAATCCTCTCGTCAAAACTC   720

 1                                10
lnGluIleCysArgAsnProValThrAspAsnValLysAspIleT
AGGAGATCTGCAGGAATCCTGTGACTGATAATGTAAAAGACATTA   765

      18
hrLysLeu
```

FIG.14B CONT.'

```
CAAAACTGGTAAGTAAAGAATGATTTTGGCATCTATAAGTCTTCC    810

CTGTGCTTGCTGACCACATAGGTTCAGGGCACTCCCGACAGGAGT    855

TCCCAGCTTTCTAAGATAAGGAATCACTGTACGAGTCTGAAGTGC    900

TTCTTCTGGGCAAATGGGAGATGCTTAGGTCATGGAGGGTTTATC    945

TGTATAACTGGCCCTTTGCACACCAACAAAGTGACTGACTGGCTT    990

TTGCCTGTTACCTACTG                                1007
```

Intervening sequence of unknown length

```
TCTCCAGTCCTGGGCATGGTATATACTTAGGCACCCAAGATTGGA    45

TTTACAACTCAAGCATTATATATTGGACAACnACGGGGTATGAGA    90

TATTAATGATATGTCAGGTTGGATGGATGAGTTTTCTCAAGAAAT    135

                                              19
                                             Val
TCTCTTGTATTTACTCACGTTTTCATTTCTTGGTCTCTGTAGGTG    180

                                    30
AlaAsnLeuProAsnAspTyrMetIleThrLeuAsnTyrValAla
GCGAATCTTCCAAATGACTATATGATAACCCTCAACTATGTCGCC    225

               39
GlyMetAspValLeu
GGGATGGATGTTTTGGTATGTAGTCCACACACTTCTGAGTTGCCT    270

TTTAGTAGCTAATGGGTGACCTGTGCTTATTCACATTGAAGACAT    315

TATTTGCTCTTTGTCGTTTTTAGATGTTGACCTATAATTTTTCCT    360

TCAAGCTGCTGCTAAGATTATCAGTGAGCATTTCAGTATGTGTTT    405

TAAGCCTACTCATTAAAAGGAAATGGCTCATCTTAGACGTAGCAA    450
```

FIG.14B CONT.'

```
CCGATGTTAATTTTTCCCCAGGCATCTCTCAGAGGGACTTGAATG                    495

TTAAAATCATGTTAAATTTCCTCCTTGGCTATGTTATTTCTCATG                    540

GCTATGTTATTCCTATTCGTATTTCATTTAAAGGGACGGAATATT                    585

TATTGTATTTCTGAACTTTTTCAGGCATGCATCCGGGTCTTTGAA                    630

TAAAA                                                            635
```

Intervening sequence of unknown length

```
CACTAAGACTCCTTCTAGTAATGTTTGTAATCCTGTCTGTATCGA                     45

ATGTCTTTGAAAACGCAGTGACTAAGCCATAAATAATCTTCCACA                     90

GAACGTCCAGTGGTTCATGAACTTTGTATGTGGGGGTGGGGCAAG                    135

AATTGTCTCACTATTGGTCAAGGAAGAGAAGGTAAGGTATGCAAG                    180

GGTGGTTTAATCTTCTTCCGTGGAAGGACAAAATCATCTATCATT                    225

TCCTCTGATCTCTATGCATTTGTTTGTTTTGAACTGAATCTGACT                    270

TGAGCAAGAGTTGGCGTCCTGTGTTCTGAGGAAACTCTTTGTCCT                    315

GCAGTCAGTGACTAAAAGTGCTGAGAGATCTGAAGAGCACTCTGA                    360

ATCTGCCATATTTTTAATAGATGCTTTGTCTTCTCTTTGAATTTC                    405

        40                                  50
      ProSerHisCysTrpLeuArgAspMetValThrHisLeu
TTCCAGCCTAGTCATTGTTGGTTACGAGATATGGTAACACACTTA                    450

                    60
SerValSerLeuThrThrLeuLeuAspLysPheSerAsnIleSer
TCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTCT                    495

        70                                  80
GluGlyLeuSerAsnTyrSerIleIleAspLysLeuGlyLysIle
```

FIG.14B CONT.'

```
GAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGGGAAAATA                    540

                                  90                    96
ValAspAspLeuValAlaCysMetGluGluAsnAlaProLys
GTGGATGACCTCGTGGCATGTATGGAAGAAAATGCACCTAAGGTA                    585

ACTTGGTATTCATCAGAATTATTTTTCTTATACT                               619

      Intervening sequence of unknown length

GAGCTCATGATGAGCAATTCACAACCACTTGTAATTCCAGCTCCA                     45

GAGGACATTATCCCCTCTTTGGATGCCATAGGAATCTGCTCTCAA                     90

ATATGTAGATACCACCTCTGCCACCTCAGCACATACATACACATA                    135

ATTAAAAAATAGAAACATTAAAGGAGTTCCAATCAATCCTTATTC                    180

TTTTCTGTATTCAGTATGCCCAGATGTAAATTCTAGGAATATGTT                    225

TTAAAGGCTAATTCTTATTTTGTAATAAGCAGCTTTAAAATTCTT                    270

AATTGTTTTTTCGGGTCACTTTATTGTCCTATTGCCACGACATTG                    315

TCCTGTCCCATTGTCTGTTATTCCTTCTGTTTTGTTTATTGTTCC                    360

CTAGTTACTTTGATCATGAGATTGACCTGTTACCCGTTGTTATTC                    405

TCTGTAGCCATTTTGAGTTGTGTCTATTAGAACAGCTGTTAAATT                    450

ACTTGAATCATTGAGGACATAGTCAATAATCTATTATGCTGATCC                    495

AGTCAAGTCTATGAGTTATTTGAAAACTAGAATCTTTGTTAATTA                    540

                                        97
                                      AsnValLys
TTTGTTTGCTTGTTTGTTTGTTTATTATTTGTCTAGAATGTAAAA                    585

100                                 110
GluSerLeuLysLysProGluThrArgAsnPheThrProGluGlu
```

FIG.14B CONT.'

GAATCACTGAAGAAGCCAGAAACTAGAAACTTTACTCCTGAAGAA 630

120

PhePheSerIlePheAsnArgSerIleAspAlaPheLysAspPhe

TTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAAGGACTTC 675

130 140

MetValAlaSerAspThrSerAspCysValLeuSerSerThrLeu

ATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTA 720

148

GlyProGluLysA

GGTCCTGAGAAAGGTAAGGCTTTTAAGCATTTCTTGTTTAAATGT 765

ACATAGAAAGCCTGAACTTCTGTAAGCCTCTACTGCTGAATCAAC 810

TAAATGTGTTGCTGTAGAAAGAACGTGTGGGTTTTTCTGATAAAA 855

ACAAAAAGCAAATATCAATGACTACCAATGATTATTATCTAGCTT 900

GAGAGATATGCCCTAAGACAGCGATTCTCGATATTTCTAAATTAA 945

AGAATTGTGTGATGGTGGCTCACATATTTTCTAACTGTGATATTT 990

GCCAGGAGAGTAGAATAATGTTATTCTTCATCCCCAGAATTCCTA 1035

AGATTTCACGTCTCATGTCTTTTCCATAAGGTTCAAACTCTGAGA 1080

CTTGAGTTCTGAGCCTCAGCAGGTCATTCTGAATCCCCACTCTCC 1125

CCGAGCTGGGTCCCTATGGGGGAACTAACTTCATTGCTTTCTTTT 1170

AAAACATGACGAGTTACCAACAGCTCCTCGCTATTATAAACATGT 1215

TCCTAAGCATGTCTGTGCATGCaATAAGCCTTCACTCTACAAGAC 1260

AGTTATGGTGTATCGCTTGACAAAACTGAGCAGCCAAGCTGAGTA 1305

TGAAATAATAATCTAGACTTGGGAGGCAGACCCAGCACCTACTGT 1350

GATATTGCACTTCGCCTTTGGGGGACTCTATGATTCAAAAGTTCA 1395

FIG.14B CONT.

```
                                                    150
                                                  spSerArgV
CCATGTAACACTGACACATTATTGCTTTCTATTTAGATTCCAGAG    1440

                                160
alSerValThrLysProPheMetLeuProProValAlaAlaSerS
TCAGTGTCACAAAACCATTTATGTTACCCCCTGTtGCAGCCAGTT    1485

        170                 176
erLeuArgAsnAspSerSerSerSerAsn_
CCCTTAGGAATGACAGCAGTAGCAGTAATAGTAAGTACACATATC    1530

TGATTTACTGCATGCATGGCTCCAAGTATCCTCTATAGGAGTGTT    1575

GCATGGACTTAAAGTTTATAAATCACTACTAATAATGCTGTTCTG    1620

TCACTGTTATTCCTTGTATGGGCTTCCTGACAATTAAATATCTGG    1665

TTTGTAGAATCGGATCTCCTTAGAGGTTAAGATGACCATGACAAA    1710

ATTAGGCCAATCAACTTTCTGCGAAGGTTATTTTAAATAAGGCAC    1755

GAAATTAATTGAAGGAAAAAAAAATACAAGCAAGGCCTTATTTTG    1800

AATCATGGTAGGCTTAAAATAGACTTTGTGGAGAATGTCCCTGAT    1845

CAAAGTGGAGTTTTCAGATTTCAAGTGCATGTGCTAACTCTCCAC    1890

AATGTCAAGGCTATTTTCAGTTTTGTGTCTCCATATTTACTACTG    1935

CATGTTTGGAAATTTGCTGATGCTGTTAGATTACCTAAGAATGTA    1980

TGTTGAAGAAGAATGGACTTCTTTCCCTAAAATTTCTGTCCTCTT    2025

TGcCCAAGAACCCAcGTTCCTGGAAGACTATCTTATTTTCATGTC    2070

TGTGCAATGATCATTATAAAGATTATTGAATATACTGGGAATACT    2115

CTGGTTTCTGTTTTTACAGATTCATAATAGCTTATTCAGTCTTTA    2160

AAGAAAGTTCTCTGAAGTCCATGCTTTAGAATGTTTCTCTATCAA    2205
```

FIG. 14B CONT.'

AACTTGACCTGGACCTTAAATAAAGCTATATTTAGTCTTTTTATC 2250

CCTGAAAAATATATTTCACAGTGTAGACATTTGATATACATCTAA 2295

GGGAAGGATGCTGCCAGAATGCTCGGGCTGGCAGTCTACAAAGTC 2340

CACTGCTCTCAGGATGGACTTCTGAAAGCGGAAATTGTGAACTGC 2385

ATGCATATAACATATCAGATCCTCGAGC 2413

FIG.14C

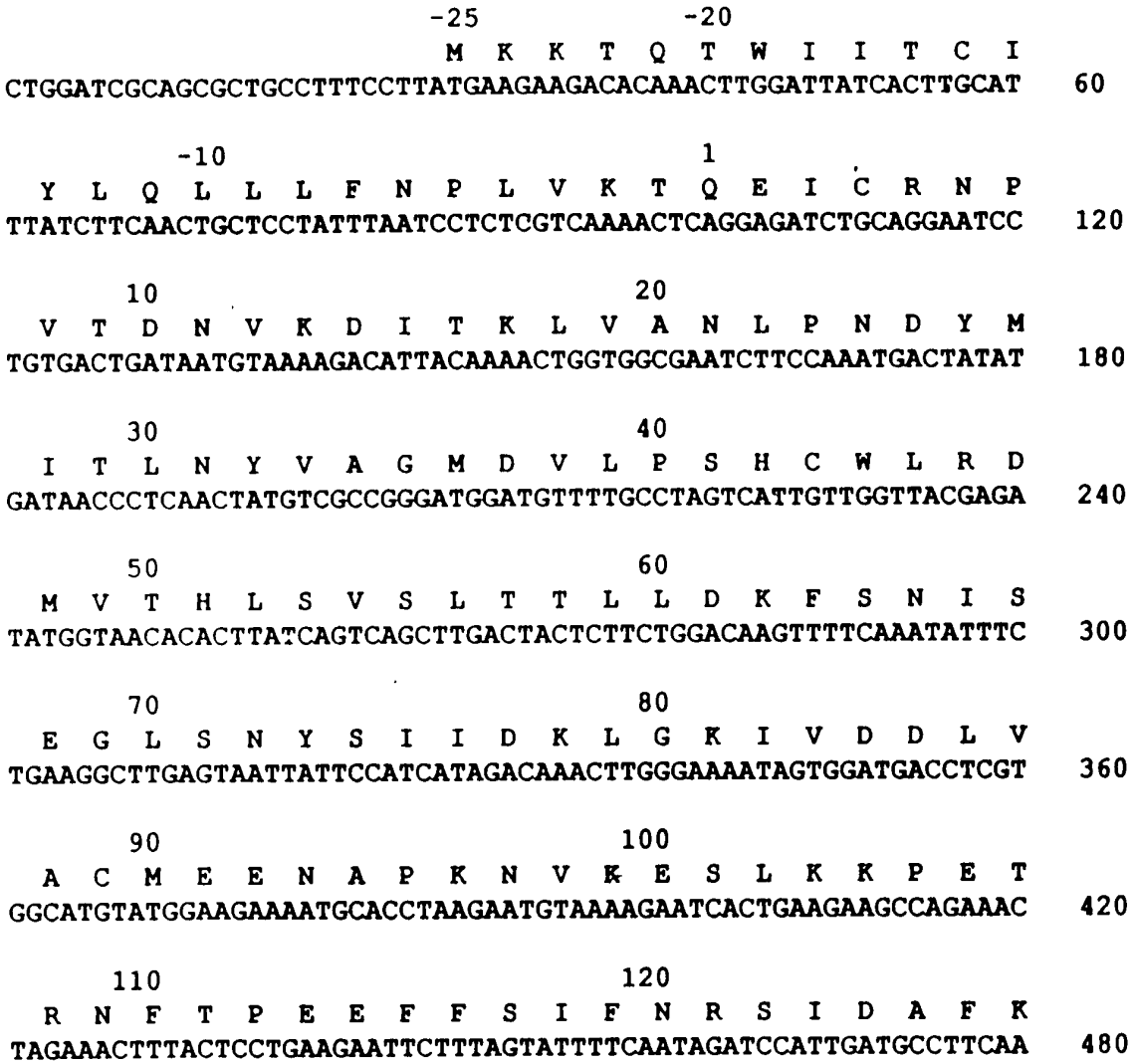

-25 -20
M K K T Q T W I I T C I
CTGGATCGCAGCGCTGCCTTTCCTTATGAAGAAGACACAAACTTGGATTATCACTTGCAT 60
-10 1
Y L Q L L L F N P L V K T Q E I C R N P
TTATCTTCAACTGCTCCTATTTAATCCTCTCGTCAAAACTCAGGAGATCTGCAGGAATCC 120
10 20
V T D N V K D I T K L V A N L P N D Y M
TGTGACTGATAATGTAAAAGACATTACAAAACTGGTGGCGAATCTTCCAAATGACTATAT 180
30 40
I T L N Y V A G M D V L P S H C W L R D
GATAACCCTCAACTATGTCGCCGGGATGGATGTTTTGCCTAGTCATTGTTGGTTACGAGA 240
50 60
M V T H L S V S L T T L L D K F S N I S
TATGGTAACACACTTATCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTC 300
70 80
E G L S N Y S I I D K L G K I V D D L V
TGAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGGGAAAATAGTGGATGACCTCGT 360
90 100
A C M E E N A P K N V K E S L K K P E T
GGCATGTATGGAAGAAAATGCACCTAAGAATGTAAAAGAATCACTGAAGAAGCCAGAAAC 420
110 120
R N F T P E E F F S I F N R S I D A F K
TAGAAACTTTACTCCTGAAGAATTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAA 480

FIG. 14C CONT.'

```
     130                                 140
  D  F  M  V  A  S  D  T  S  D  C  V  L  S  S  T  L  G  P  E
GGACTTCATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTAGGTCCTGA   540

     150                                 160
  K  D  S  R  V  S  V  T  K  P  F  M  L  P  P  V  A  A  S  S
GAAAGATTCCAGAGTCAGTGTCACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGTTC   600

     170                                 180
  L  R  N  D  S  S  S  S  N  R  K  A  A  K  S  P  E  D  P  G
CCTTAGGAATGACAGCAGTAGCAGTAATAGGAAAGCCGCAAAGTCCCCTGAAGACCCAGG   660

     190                                 200
  L  Q  W  T  A  M  A  L  P  A  L  I  S  L  V  I  G  F  A  F
CCTACAATGGACAGCAATGGCACTGCCGGCTCTCATTTCGCTTGTAATTGGCTTTGCTTT   720

     210                                 220
  G  A  L  Y  W  K  K  K  Q  S  S  L  T  R  A  V  E  N  I  Q
TGGAGCCTTATACTGGAAGAAGAAACAGTCAAGTCTTACAAGGGCAGTTGAAAATATACA   780

     230                                 240
  I  N  E  E  D  N  E  I  S  M  L  Q  Q  K  E  R  E  F  Q  E
GATTAATGAAGAGGATAATGAGATAAGTATGTTGCAACAGAAAGAGAGAGAGTTTCAAGA   840

248
  V
GGTGTAATT                                                      849
```

FIG.15A

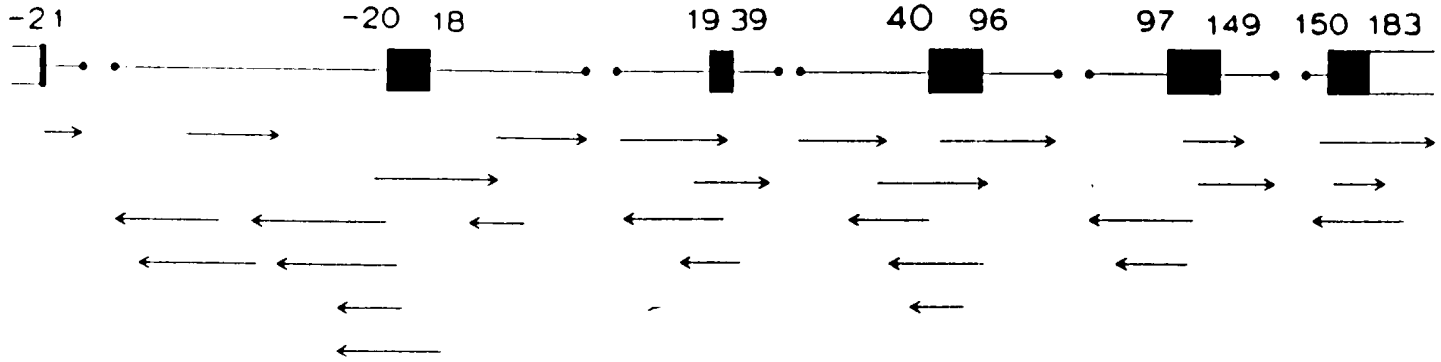


FIG.15B

-21
hrGln

CACAAGTGAGTAGGGCGCGCCCGGGAGCTCCCAGGCTCTCCAGGA 45

AAAATCGCGCCCGGTGCCCCGGGGaAGCCGGCGCTCCCTGGGACT 90

TGCAGCTGGGGCGTGCAGGGCTGTGCCTGCCGGGTG 126

Intervening sequence of unknown length

AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTA 45

CAGTGTAATAAGGAAAAATAAGTCATGCATAAAAGCAACTATAAT 90

ACATAATAGAAAATGTTATTTTCAAGCCGATGTGTAGGTTATGTG 135

TGTTCGAGAGAGAGAGAGAAGACAGATTACTTTCTGCTAGGGT 180

TCAAGAATGCCTTCCTGTTGGCTAAGGAAATATTTTCCTTAAGTG 225

GCTAAAAAGCTGTGTTTCAAAATATTCTTTTGATGTCTCACAAAT 270

TCAGTGGAATTCTCTTAGGTCTAAAAATATACATCTCTCTCACTT 315

TAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA 360

GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAA 405

ATAAGATGTTTCTTTTGGTGCCATAAGGTATACATTTTATGCATT 450

CTCTAGTTTTTAGAAGATACCCTAAGGGCTAAGTCTTTAACATGC 495

TGCTACAAGTTTATTCCTAATTGCCATTGGGAAATTGGCTGAAGA 540

AAGTTTTTAACAAAAGTTAACAATATTGTCATTGAGAGAATAATT 585

CAAAATGGATTTTAACTAAAAGCTTTTAAAAACTTTGGTGAGCAT 630

AGCTTGAATGCGTAATATTTAATTGCATTTAAGCCAATAACATAT 675

FIG.15B CONT.'

```
ATTAGACTGGTCTTTTTGTGCATCAAGGCATTAGATGTTAAAAGT    720

TTGAATGATTACAGATCTTAACTGATGATCACCAAGCAATTTTTC    765

                -20                          -10
                ThrTrpIleLeuThrCysIleTyrLeuGlnLe
TGTTTTCATTTAGACTTGGATTCTCACTTGCATTTATCTTCAGCT    810

                                  1
uLeuLeuPheAsnProLeuValLysThrGluGlyIleCysArgAs
GCTCCTATTTAATCCTCTCGTCAAAACTGAAGGGATCTGCAGGAA    855

            10                          18
nArgValThrAsnAsnValLysAspValThrLysLeu
TCGTGTGACTAATAATGTAAAAGACGTCACTAAATTGGTAAGTAA    900

GGAATGCTTTACCGTGCTGTGTAAAAAAGAGCTGTGGCTCTTTTT    945

CCTGTGCTTGTTGATAAAAGATTTAGATTTTTCTTGCCCCAAAGT    990

AATGTTTTCCTAAAGTGGGGAAAGTAATCACTGGGTTACAATAAA   1035

GGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA   1080

TTTGTTGGTAAAACTGGCTAGTTGCACACCACTGCTGTGACTGCT   1125

TCTTTGCTGGTCTTCTCCCCATCCTTCATAGGCAGTGAAGGACCT   1170

TGGAGAGTTCGCTGTGTGCTGATGGGCTTGCCCCAGCTTGTTCCC   1215

CATAATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTCCCCTTCA   1260

CATGTCTTCCTACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCT   1305

GAAATGGCTATTCTCCCAATTCAATCAGCAGGAAGACCCTGTCAC   1350

ATGTCAGTGGGTGTTTGCTCCTTCAGGGAACATAGAGAGGTGATT   1395

CATTGCCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTCACAT   1440

TGAACTCTTCCCTCAGCGAAAGCATTTGCATTGCTTCCC         1479
```

FIG.15B CONT.'

Intervening sequence of unknown length

```
GAATTCCAAGATCACAGGTGGAAGCTGAAATTCAGATCATGTTTC    45

CAAAACTCAGTAGGTTATACCTAGCCAGGCATAACTGAATTTGGA    90

GTCTAAAAGATCTGTATTATCACTTTTTTATTTTGAAGGATGCCT   135

TTTGATTACAGAGGGAAATCAAGGATTAAAAATCAATATACATGT   180

AAATATTGAAATTCATTGGTAACTTTAAAAAGCACAACAGTTTTG   225

TGTGCTTTTCTCCAAAGCACTACAAATATGATTAATTGATGTATA   270

                                          19
                                       ValAlaA
AGAATTTTCTTATGGAATTTTTTTTTTTGTCTCTGTAGGTGGCAA   315

                                   30
snLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM
ATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGA   360

          39
etAspValLeu
TGGATGTTTTGGTATGTAAACTACATTTCTGAGTTTCATTTTAGT   405

AGCTCATAGAAGAAATGGGATCATTCATATTGAGATAGTACACTA   450

GCTGCTATTTAGGAGCTTGCTTATTGTCAGGATTTGAAGAATTTA   495

TCTTTGGAATTTGACTTGCAGGCTTTTTTTTCCCCCTCTT  535
```

Intervening sequence of unknown length

```
CCTGTTACAAGAGTCCCTCCTCCTATTACAATAGTCCCTCCTCCT    45

CCTGTCACACTAGTCCCTTCTCTTCCTGTTACAATAACCCCTGTC    90
```

FIG.15B CONT.'

```
CTCCTATTACAACATTTTAAGTAATGTAATATTAATTTTAAAAAT   135

CTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG   180

AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAG   225

CCTGGCCAACATGGTGAAACTTCCTCTCTACTAAAAATAAAAAAG   270

TAGCCAGGCATGGTGGCAGGCACTTGTAATCTGAGCTACTCGAGA   315

GGCTGAGGCAGGAGAATCACTTGAGTAACTAAAACGATAGCTTTG   360

AAGAGTACTCCGAGTTTTATGGCACTTACTTATTAAAATAGCTGT   405

                                40
                              ProSerHisCysTrpIleS
TTTGTCTCTTTTTTCATATCTTGCAGCCAAGTCATTGTTGGATAA   450

              50                                60
erGluMetValValGlnLeuSerAspSerLeuThrAspLeuLeuA
GCGAGATGGTAGTACAATTGTCAGACAGCTTGACTGATCTTCTGG   495

                                70
spLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI
ACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA   540

              80                                90
leAspLysLeuValAsnIleValAspAspLeuValGluCysValL
TAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTGA   585

                  96
ysGluAsnSerSerLys
AAGAAAACTCATCTAAGGTAACTTTGTGTTCATTGGGATTATTTT   630

TCATTACGCTTCTCTAAAAACCCATGCTTCTTGGTGCTGTTGGGG   675

AAAATGAGGCACCTTTATTTATGATATTTTGATTGTATAAACTTC   720

AAATTTAAAAATCTTGTTCAGATGAGCAAAGAAAACAAGTATTTG   765

CAGTTATACTGCAATACTGAAGTGCACATTC   796
```

FIG.15B CONT.'

Intervening sequence of unknown length

```
TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCA    45

CTACCCTGCATTACCAATCTGAATTACATACGTTAAAACAGCCAT    90

CTAAAAGTGCTAGTTGTAAGAGTCTAAATACTTGAATCTTTGAGA   135

GACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA   180

                                        97
                                      AspLeuLysL
CTATTTGAAAAATGTAATCCTATTTTTTCTTCTAGGATCTAAAAA   225

                              110
ysSerPheLysSerProGluProArgLeuPheThrProGluGluP
AATCATTCAAGAGCCCAGAACCCAGGCTCTTTACTCCTGAAGAAT   270

          120                                130
hePheArgIlePheAsnArgSerIleAspAlaPheLysAspPheV
TCTTTAGAATTTTTAATAGATCCATTGATGCCTTCAAGGACTTTG   315

                                   140
alValAlaSerGluThrSerAspCysValValSerSerThrLeuS
TAGTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAA   360

     148
erProGluLysA
GTCCTGAGAAAGGTAAGACATGTAAGCATTTCCAGTTCAAATGTA   405

AACAACAAACTTAAATCTTCCCTATGTAGTAAGAATCTACCTCTG   450

TGTTAAGCTGTAGCAAGATACATGCATGTACGTCTAATAAAAAAG   495

CAGATATCAATAGCACAGAAGAAA                        519
```

Intervening sequence of unknown length

FIG.15B CONT.'

```
CTCTATAACTCATACAAATCACCATATAACACTGACACATTATTG    45

                150                          160
             spSerArgValSerValThrLysProPheMetL
CTTTCTATTTAGATTCCAGAGTCAGTGTCACAAAACCATTTATGT    90

                                170
euProProValAlaAlaSerSerLeuArgAsnAspSerSerSerS
TACCCCCTGTTGCAGCCAGCTCCCTTAGGAATGACAGCAGTAGCA   135

  176
erAsnA
GTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA    180

ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCT    225

ACATTTATTATTATTGATACTGTTCTGTTACTGTTATTCCTTTTA    270

TGGTCTTCTTGAGACTTAAGTTTGTAGAATTAAATTTCCCTAGAG    315

CTGGAGATAATGTTTAGAGAATTAGGCCAATAAATTT            352
```

FIG.15C

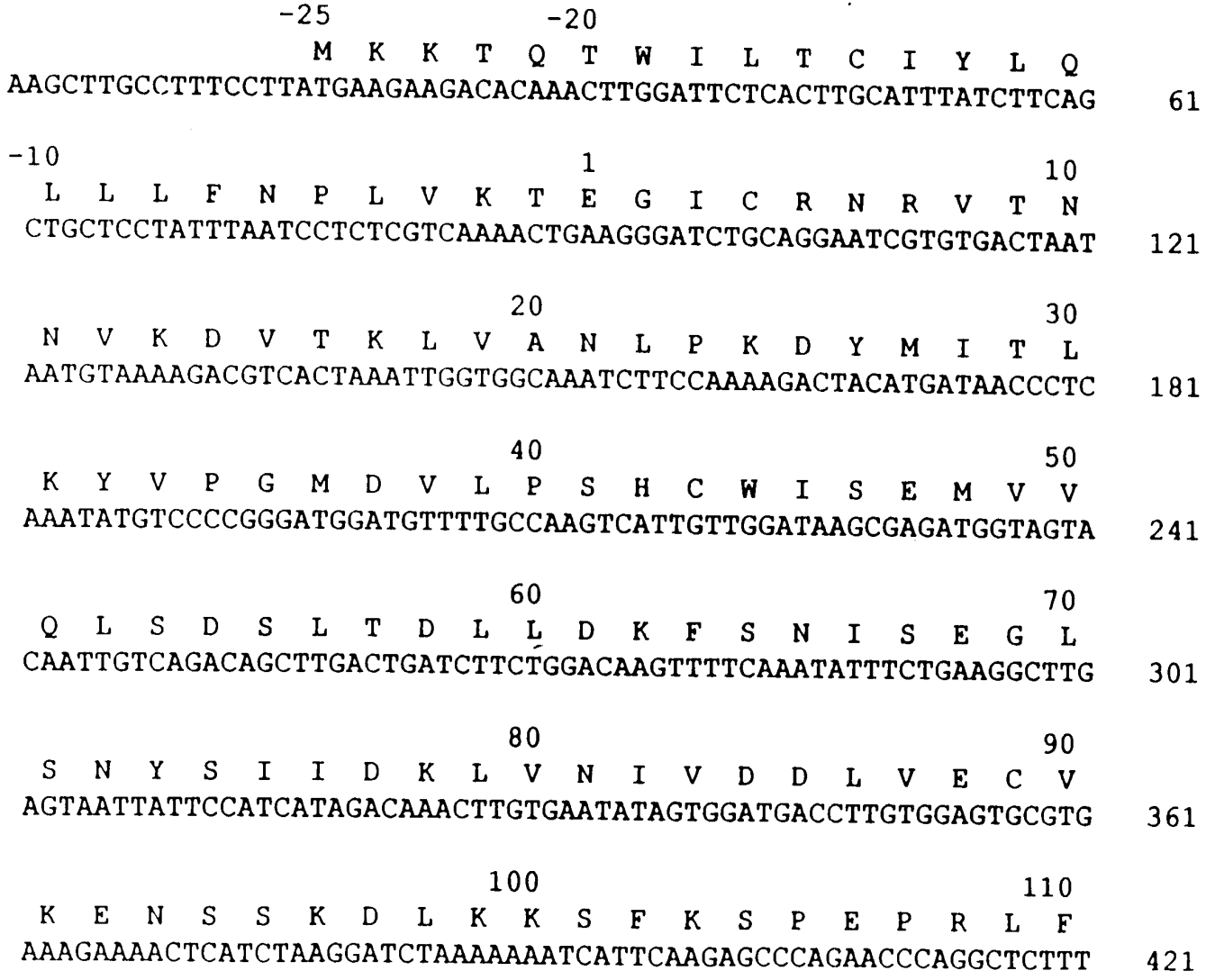

-25 -20
M K K T Q T W I L T C I Y L Q
AAGCTTGCCTTTCCTTATGAAGAAGACACAAACTTGGATTCTCACTTGCATTTATCTTCAG 61
-10 1 10
L L L F N P L V K T E G I C R N R V T N
CTGCTCCTATTTAATCCTCTCGTCAAAACTGAAGGGATCTGCAGGAATCGTGTGACTAAT 121
20 30
N V K D V T K L V A N L P K D Y M I T L
AATGTAAAAGACGTCACTAAATTGGTGGCAAATCTTCCAAAAGACTACATGATAACCCTC 181
40 50
K Y V P G M D V L P S H C W I S E M V V
AAATATGTCCCCGGGATGGATGTTTTGCCAAGTCATTGTTGGATAAGCGAGATGGTAGTA 241
60 70
Q L S D S L T D L L D K F S N I S E G L
CAATTGTCAGACAGCTTGACTGATCTTCTGGACAAGTTTTCAAATATTTCTGAAGGCTTG 301
80 90
S N Y S I I D K L V N I V D D L V E C V
AGTAATTATTCCATCATAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTG 361
100 110
K E N S S K D L K K S F K S P E P R L F
AAAGAAAACTCATCTAAGGATCTAAAAAAATCATTCAAGAGCCCAGAACCCAGGCTCTTT 421

FIG.15C CONT.'

```
                                120                                 130
 T  P  E  E  F  F  R  I  F  N  R  S  I  D  A  F  K  D  F  V
ACTCCTGAAGAATTCTTTAGAATTTTTAATAGATCCATTGATGCCTTCAAGGACTTTGTA    481

                                140                                 150
 V  A  S  E  T  S  D  C  V  V  S  S  T  L  S  P  E  K  D  S
GTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAAGTCCTGAGAAAGATTCC    541

                                160                                 170
 R  V  S  V  T  K  P  F  M  L  P  P  V  A  A  S  S  L  R  N
AGAGTCAGTGTCACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGCTCCCTTAGGAAT    601

                                180     183
 D  S  S  S  S  N  S  K  Y  I  Y  L  I
GACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCAAT    661

TAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCTACATTTATTATTATTGA    721

TACTGTTCTGTTACTGTTATTCCTTTTATGGTCTTCTTGAGACTTAAGTTTGTAGAATTA    781

AATTTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGG                         820
```


GAGCTCCGAGCcCTCtCTGGCGCgCgAGGTATTTCGTCTGTnCCCGGGGGTGCCAGGTGA 60
GCCCCAGCGGATCCGGGAGGGTAAGCTGGGACTCCTCGCGAGCAGTAGCTGCAGGGTACC 120
AAGCTTCGCCCTCTGCGTCCCCGCGCCTTCGCGGTCTCCCGCCAGTGCAGGTCCGGGGCC 180
CCCAGGCGAGCGGACAAGGTTGGCCTAATCTGCCAAACTTCTGGGGCATTTACCGTGCTC 240
TGGCCGCCCTCCCGATTCTTCCCTCCGCGCCCTTGCCTGCTTCTCGCCTACCCCGGGCTC 300
CGGAAGGGAAGGAGGCGTGTCCGGAGCAGGCGGGCGGGAACTGTATAAAAGCGCCGGCGG 360
CTCAGCAGCCGGCTTCGCTCGCCGCCTCGCGCCGAGACTAGAAGCGCTGCGGGAAGCAGG 420
GACAGTGGAGAGGGCGCTGCGCTCGGGCTACCCAATGCGTGGACTATCTGCCGCCGCTGT 480
TCGTGCAAC[illegible]GCTGGAGCTCCAGAACAGCTAAACGGAGTCGCCACACCACTGTTTGTGC 540
-25 -21
MetLysLysThrGln
TGGATCGC[illegible]GTGCCTTTCCTTATGAAGAAGACACAAGTGAGTAGGGCGCGCCCGGGA 600
GCTCCCAGGCTC[illegible]CCAGGAAAAATCGCGCCCGGTGCCCCGGGGAAGCCGGCGCTCCCTGG 660
GACTTGCAGC[illegible]GGGGCGTGCAGGGCTGTGCCTGCCGGGTGAGACAAGAGGATGCGGGGGA 720
GGCCGGCGTGG[illegible]GTGTGATCCCGAGCCGAGCCGnnTGAGCCAGGGAGAAAAGGAGTGGGA 780
GTnCTGAGAGGGAGCCAGTGTCAAGTTTGGAGCCTCAGCAGTTAAGTTTTGAGCTGTCAG 840
TCGGAAACCGTAATTCCCGTCTGGTGGAAAGATTGGCTTTTnGnCCACGGAATGTAAGTT 900
ATCAC 905

FIG. 15D

Intervening sequence of unknown length

AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTACAGTGTAATAAGGAA 60

AAATAAGTCATGCATAAAAGCAACTATAATACATAATAGAAAATGTTATTTTCAAGCCGA 120

TGTGTAGGTTATGTGTGTTCGAGAGAGAGAGAGAGAAGACAGATTACTTTCTGCTAGGGT 180

TCAAGAATGCCTTCCTGTTGGCTAAGGAAATATTTTCCTTAAGTGGCTAAAAAGCTGTGT 240

TTCAAAATATTCTTTTGATGTCTCACAAATTCAGTGGAATTCTCTTAGGTCTAAAAATAT 300

ACATCTCTCTCACTTTAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA 360

GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAAATAAGATGTTTCTTT 420

TGGTGCCATAAGGTATACATTTTATGCATTCTCTAGTTTTTAGAAGATACCCTAAGGGCT 480

AAGTCTTTAACATGCTGCTACAAGTTTATTCCTAATTGCCATTGGGAAATTGGCTGAAGA 540

AAGTTTTTAACAAAAGTTAACAATATTGTCATTGAGAGAATAATTCAAAATGGATTTTAA 600

CTAAAAGCTTTTAAAAACTTTGGTGAGCATAGCTTGAATGCGTAATATTTAATTGCATTT 660

AAGCCAATAACATATATTAGACTGGTCTTTTTGTGCATCAAGGCATTAGATGTTAAAAGT 720

-20

Th

TTGAATGATTACAGATCTTAACTGATGATCACCAAGCAATTTTTCTGTTTTCATTTAGAC 780

-10

rTrpIleLeuThrCysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrGl

TTGGATTCTCACTTGCATTTATCTTCAGCTGCTCCTATTTAATCCTCTCGTCAAAACTGA 840

FIG. 15D CONT.

1 10 18

uGlyIleCysArgAsnArgValThrAsnAsnValLysAspValThrLysLeu

AGGGATCTGCAGGAATCGTGTGACTAATAATGTAAAAGACGTCACTAAATTGGTAAGTAA 900

GGAATGCTTTACCGTGCTGTGTAAAAAAGAGCTGTGGCTCTTTTTCCTGTGCTTGTTGAT 960

AAAAGATTTAGATTTTTCTTGCCCCAAAGTAATGTTTTCCTAAAGTGGGGAAAGTAATCA 1020

CTGGGTTACAATAAAGGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA 1080

TTTGTTGGTAAAACTGGCTAGTTGCACACCACTGCTGTGACTGCTTCTTTGCTGGTCTTC 1140

TCCCCATCCTTCATAGGCAGTGAAGGACCTTGGAGAGTTCGCTGTGTGCTGATGGGCTTG 1200

CCCCAGCTTGTTCCCCATAATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTCCCCTTCA 1260

CATGTCTTCCTACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCTGAAATGGCTATTCTC 1320

CCAATTCAATCAGCAGGAAGACCCTGTCACATGTCAGTGGGTGTTTGCTCCTTCAGGGAA 1380

CATAGAGAGGTGATTCATTGCCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTCACAT 1440

TGAACTCTTCCCTCAGCGAAAGCATTTGCATTGCTTCCC 1479

Intervening sequence of unknown length

GAATTCCAAGATCACAGGTGGAAGGTGAAATTCAGATCATGTTTCCAAAACTCAGTAGGT 60

TATACCTAGCCAGGCATAACTGAATTTGGAGTCTAAAAGATCTGTATTATCACTTTTTTA 120

TTTTGAAGGATGCCTTTTGATTACAGAGGGAAATCAAGGATTAAAAATCAATATACATGT 180

FIG. 15D CONT.

AAATATTGAAATTCATTGGTAACTTTAAAAAGCACAACAGTTTTGTGTGCTTTTCTCCAA 240

AGCACTACAAATATGATTAATTGATGTATAAGAATTTTCTTATGGAATTTTTTTTTTTGT 300

19 30

ValAlaAsnLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM

CTCTGTAGGTGGCAAATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGA 360

39

etAspValLeu

TGGATGTTTTGGTATGTAAACTACATTTCTGAGTTTCATTTTAGTAGCTCATAGAAGAAA 420

TGGGATCATTCATATTGAGATAGTACACTAGCTGCTATTTAGGAGCTTGCTTATTGTCAG 480

GATTTGAAGAATTTATCTTTGGAATTTGACTTGCAGGCTTTTTTTTCCCCCTCTT 535

Intervening sequence of unknown length

CCTGTTACAAGAGTCCCTCCTCCTATTACAATAGTCCCTCCTCCTCCTGTCACACTAGTC 60

CCTTCTCTTCCTGTTACAATAACCCCTGTCCTCCTATTACAACATTTTAAGTAATGTAAT 120

ATTAATTTTAAAAATCTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG 180

AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAGCCTGGCCAACATGGT 240

GAAACTTCCTCTCTACTAAAAATAAAAAAGTAGCCAGGCATGGTGGCAGGCACTTGTAAT 300

CTGAGCTACTCGAGAGGCTGAGGCAGGAGAATCACTTGAGTAACTAAAACGATAGCTTTG 360

AAGAGTACTCCGAGTTTTATGGCACTTACTTATTAAAATAGCTGTTTTGTCTCTTTTTTC 420

FIG. 15D CONT.

```
          40                                  50
        ProSerHisCysTrpIleSerGluMetValValGlnLeuSerAspSerL
ATATCTTGCAGCCAAGTCATTGTTGGATAAGCGAGATGGTAGTACAATTGTCAGACAGCT    480

          60                                  70
euThrAspLeuLeuAspLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI
TGACTGATCTTCTGGACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA    540

          80                                  90
leAspLysLeuValAsnIleValAspAspLeuValGluCysValLysGluAsnSerSerL
TAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTGAAAGAAAACTCATCTA    600
96
ys
AGGTAACTTTGTGTTCATTGGGATTATTTTTCATTACGCTTCTCTAAAAACCCATGCTTC    660

TTGGTGCTGTTGGGGAAAATGAGGCACCTTTATTTATGATATTTTGATTGTATAAACTTC    720

AAATTTAAAAATCTTGTTCAGATGAGCAAAGAAAACAAGTATTTGCAGTTATACTGCAAT    780

ACTGAAGTGCACATTC                                                 796

                Intervening sequence of unknown length

TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCACTACCCTGCATTACC     60

AATCTGAATTACATACGTTAAAACAGCCATCTAAAAGTGCTAGTTGTAAGAGTCTAAATA    120

CTTGAATCTTTGAGAGACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA    180

                                    97
                                  AspLeuLysLysSerPheLysSerP
CTATTTGAAAAATGTAATCCTATTTTTTCTTCTAGGATCTAAAAAAATCATTCAAGAGCC    240
```

FIG. 15D CONT.

```
                110                                 120
roGluProArgLeuPheThrProGluGluPhePheArgIlePheAsnArgSerIleAspA
CAGAACCCAGGCTCTTTACTCCTGAAGAATTCTTTAGAATTTTTAATAGATCCATTGATG    300

                130                                 140
laPheLysAspPheValValAlaSerGluThrSerAspCysValValSerSerThrLeuS
CCTTCAAGGACTTTGTAGTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAA    360

         148
erProGluLysA
GTCCTGAGAAAGGTAAGACATGTAAGCATTTCCAGTTCAAATGTAAACAACAAACTTAAA    420

TCTTCCCTATGTAGTAAGAATCTACCTCTGTGTTAAGCTGTAGCAAGATACATGCATGTA    480

CGTCTAATAAAAAAGCAGATATCAATAGCACAGAAGAAACTAATGATTGTAGATTTGTGGG   541

                    Intervening sequence of unknown length

                                                                spS
CTCTATAACCCATACAAATCACCATATAACACTGACACATTATTGCTTTCTATTTAGATT    60

150                             160
erArgValSerValThrLysProPheMetLeuProProValAlaAlaSerSerLeuArgA
CCAGAGTCAGTGTCACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGCTCCCTTAGGA    120

170             176
snAspSerSerSerSerAsnA
ATGACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA    180

ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCTACATTTATTATTATT    240

GATACTGTTCTGTTACTGTTATTCCTTTTATGGTCTTCTTGAGACTTAAGTTTGTAGAAT    300
```

FIG. 15D

TAAATTTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGGCCAATAAATTTTCTGCTGA 360

GGTTATTTTAAATAAGACATAAAATTAATTTTAGAAATATGATTTATGCCTTTTGTTGAA 420

TCATTAACATATAT 434

Intervening sequence of unknown length

ACAGAAACAGTTAAAACAACCACAGCATAAGAGnAAAACTTCTAGAATGGATATGCTGTA 60

178

rgLysAlaLysAsnProProGlyAspSerSerL

TTCATCAGTGTGTTCTTTAAATTATAGGGAAGGCCAAAAATCCCCCTGGAGACTCCAGCC 120

190 200

euHisTrpAlaAlaMetAlaLeuProAlaLeuPheSerLeuIleIleGlyPheAlaPheG

TACACTGGGCAGCCATGGCATTGCCAGCATTGTTTTCTCTTATAATTGGCTTTGCTTTTG 180

213

lyAlaLeuTyrTrpLys

GAGCCTTATACTGGAAGGTAAGTGGTACCATTCCTTtTTTTAAAAATATGCTATGTtTAC 240

ATAAATTATCATCTTTTTTTCCTCAAGAAATGATCCTTtAAGAAAACAGTGAATCTACCT 300

TAGCTTATACTAAACAAAATTTAAATTTTATAAAGTTTCCTGTTTCTCATTATGTCTGGA 360

GACAATCCCTCTAGCTGATAATTCACGCTTAAGAATTAGGAACT 404

Intervening sequence of unknown length

FIG. 15D CONT.

```
AAAACTGTTATTGGAGTTATTGCCATAAAAGATAAAAGTGGAGTCCACTTACCTCTTAAA    60
                                                      214
                                                      LysArgG
TATTAGACCATTCATTGATTATTTTACAGTATATGTCTTTCTTCTTTTTCCAGAAGAGAC    120

          220                             230             235
lnProSerLeuThrArgAlaValGluAsnIleGlnIleAsnGluGluAspAsnGluIleS
AGCCAAGTCTTACAAGGGCAGTTGAAAATATACAAATTAATGAAGAGGATAATGAGATAA    180

e
GGTATTTTGTTTTGCTAAATGTGTgCCCAATCAAGCATGACATTGCCATTTCACACACTG    240

TGTACCTGCCCATAATGTCTTTAAGAAGTCCTTCACTCATGACAGTAGCTCCTAACCAGT    300

GAGTCCCAACTCTATCCATGTTTCTGATGTCTCACTCTCTCTTC                    344

                    Intervening sequence of unknown length

GTATGTGTATATGCATATACAGAGAAAGAAATGTTTTAACTACTTGGAAAGACTACCTTA    60

AGACAAATGAAGTCTTCCCTCTTCCCTATAGTAATAAGAAGGTAGGCTCCCCCATTCAAT    120

TTTGCAATCTTCTGCTACTATATTTACAGAAAAGCTGCCTTTTACAATGCCGAGATCATG    180

                                                      rM
GTGTACCTCAGAATCTCTGACCAAGAGCAAATAAGCATTTtTTCTTATTGTTTTTCAGTA    240

237                                 248
etLeuGlnGluLysGluArgGluPheGlnGluVal
TGTTGCAAGAGaAAGAGAGAGAGTTTCAAGAAGTGTAATTGTGGCTTGTATCAACACTGT    300

TACTTTCGTACATTGGTAAGTTTTTTTCTTCTTTCCTTTTTTTTTCTTTTTTTTATTATA    360
```

FIG. 15D CONT.

CTTTAAGTTCTAGGGTACATGTGCACAATGTGCAGGTTTGTTACGTATGTTTACATGTGC 420

CATGTT 426

FIG. 15D CONT.

FIG.16A

```
          -25                                                                25
Human     MKKTQTWILT CIYLQLLLFN PLVKTEGICR NRVTNNVKDV TKLVANLPKD
Monkey    MKKTQTWILT CIYLQLLLFN PLVKTEGICR NRVTNNVKDV TKLVANLPKD
Dog       MKKTQTWIIT CIYLQLLLFN PLVKTKGICG KRVTDDVKDV TKLVANLPKD
Cat       MKXTQTWIVT CIYLQXLLFN PLVKTKGLCR NRVTDDVKDV TKLVANLPKD
Cow       MKKTQTWIIT CIYLQLLLFN PLVHTQGICS NRVTDDVKDV TKLVANLPKD
Rat       MKKTQTWIIT CIYLQLLLFN PLVKTQEICR NPVTDNVKDI TKLVANLPND
Mouse     MKKTQTWIIT CIYLQLLLFN PLVKTKEICG NPVTDNVKDI TKLVANLPND
Chicken        TWIIT CFCLQLLLLN PLVKAQSSCG NPVTDDVNDI AKLVGNLPND
Scfpep    MKkTQTWIiT CiyLQlLLfN PLVkt.giCr nrVTd.VkDv tKLVaNLPkD

          26                                                                 72
Human     YMITLKYVPG MDVLPSHCWI SEMVVQLSDS LTDLLDKFSN ISEG...LSN
Monkey    YMITLKYVPG MDVLPSHCWI SEMVVQLSDS LTDLLDKFSN ISEG...LSN
Dog       YKIALKYVPG MDVLPSHCWI SVMVEQLSVS LTDLLDKFSN ISEG...LSN
Cat       YKIALKYVPG MDVLPSHCWI SVMVEQLSVS LTDLLDKFSN ISEG...LSN
Cow       YMITLKYVPG MDVLPSHCWI SEMVEQLSVS LTDLLDKFSN ISEG...LSN
Rat       YMITLNYVAG MDVLPSHCWL RDMVTHLSVS LTTLLDKFSN ISEG...LSN
Mouse     YMITLNYVAG MDVLPSHCWL RDMVIQLSLS LTTLLDKFSN ISEG...LSN
Chicken   YLITLKYVPK MDSLPNHCWL HLMVPEFSRS LHNLLQKFSD ISDMSDVLSN
Scfpep    YmItLkYVpg MDvLPsHCWi seMVeqlSvS LtdLLdKFSn ISeg...LSN

          73                                                                121
Human     YSIIDKLVNI VDDLVECVKE NSSKD.LKKS FKSPEPRLFT PEEFFRIFNR
Monkey    YSIIDKLVNI VDDLVECVKE NSSKD.LKKS FKSPEPRLFT PEEFFRIFNR
Dog       YSIIDKLVKI VDDLVECTEG YSFEN.VKKA PKSPELRLFT PEEFFRIFNR
Cat       YSIIDKLVKI VDDLVECVEG HSSEN.VKKS SKSPEPRLFT PEEFFRIFNR
Cow       YCIIDKLVKI VDDLVECMEX HSSEN.VKKS SKSPEPRQFT PEKFFGIFNK
Rat       YSIIDKLGKI VDDLVACMEE NAPKN.VKES LKKPETRNFT PEEFFSIFNR
Mouse     YSIIDKLGKI VDDLVLCMEE NAPKN.IKES PKRPETRSFT PEEFFSIFNR
Chicken   YSIINNLTRI INDLMACLAF DKNKDFIKEN GHLYEEDRFI PENFFRLFNS
Scfpep    YsIIdkLvkI vdDLveC.ee nsskn.vKks .kspEprlFt PEeFFriFNr
```

FIG.16B

```
      122                                                        169
Human  SIDAFKDF.V VASETSDCVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
Monkey SIDAFKDF.A VASETSDCVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
  Dog  SIDAFKDLET VASKSSECVV SSTL.SPDKD SRVSVTKPFM LPPVAASSLR
  Cat  SIDAFKDLEM VASKTSECVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
  Cow  SIDAFKDLEI VASKMSECVI SSTS.SPEKD SRVSVTKPFM LPPVAASSLR
  Rat  SIDAFKDF.M VASDTSDCVL SSTL.GPEKD SRVSVTKPFM LPPVAASSLR
Mouse  SIDAFKDF.M VASDTSDCVL SSTL.GPEKD SRVSVTKPFM LPPVAASSLR
Chicken TIEVYKEFAD SLDK.NDCIM PSTVETPEND SRVAVTKTIS FPPVAASSLR
Scfpep sIdafKdf.m vasktsdCvv sSTl.sPekD SRVsVTKpfm lPPVAASSLR

      170                                                        213
Human  NDSSSSNRKA KNPPGD.... ..SSLHWAAM ALPALFSLII GFAFGALYWK
Monkey NDSSSSNRKA KNPTGD.... ..SSLHWAAM ALPAFFSLII GFAFGALYWK
  Dog  NDSSSSNRKA SNSIGD.... ..SNLQWAAM ALPAFFSLVI GFAFGALYWK
  Cat  NDSSSSNRKX TNPIED.... ..SSIQWAVM ALPACFSLVI GFAFGAFYWK
  Cow  NDSSSSNRKA SNSIED.... ..SSLQWAAV ALPAFFSLVI GFAFGAFYWK
  Rat  NDSSSSNRKA AKSPED.... ..PGLQWTAM ALPALISLVI GFAFGALYWK
Mouse  NDSSSSNRKA AKAPED.... ..SGLQWTAM ALPALISLVI GFAFGALYWK
Chicken NDSIGSNTSS NSNKEALGFI SSSSLQGISI ALTSLLSLLI GFILGAIYWK
Scfpep NDSssSNrka .n..ed.... ..sslqwaam ALpalfSLvI GFafGAlYWK

      214                                                  248
Human  KRQPSLTRAV ENIQIN...E EDNEISMLQE KEREFQEV
Monkey KRQPSLTRAV ENIQIN...E DDNEISMLQE KEREFQEV
  Dog  KKQPNLTRTV ENIQIN...E EDNEISMLQE KEREFQEV
  Cat  KKQPNLTRTV ENIQIN...E EDNEISMLQE KEREFQEV
  Cow  KKQPNLTRTV ENRQIN...E EDNEISMLQE KEREFQEV
  Rat  KKQSSLTRAV ENIQIN...E EDNEISMLQQ KEREFQEV
Mouse  KKQSSLTRAV ENIQIN...E EDNEISMLQQ KEREFQEV
Chicken KTHPKSRPES NETIQCHGCQ EENEISMLQQ KEKEHLQV
Scfpep Kkqpsltrav eniqin...e edNEISMLQe KErEfqeV
```

FIG. 16C

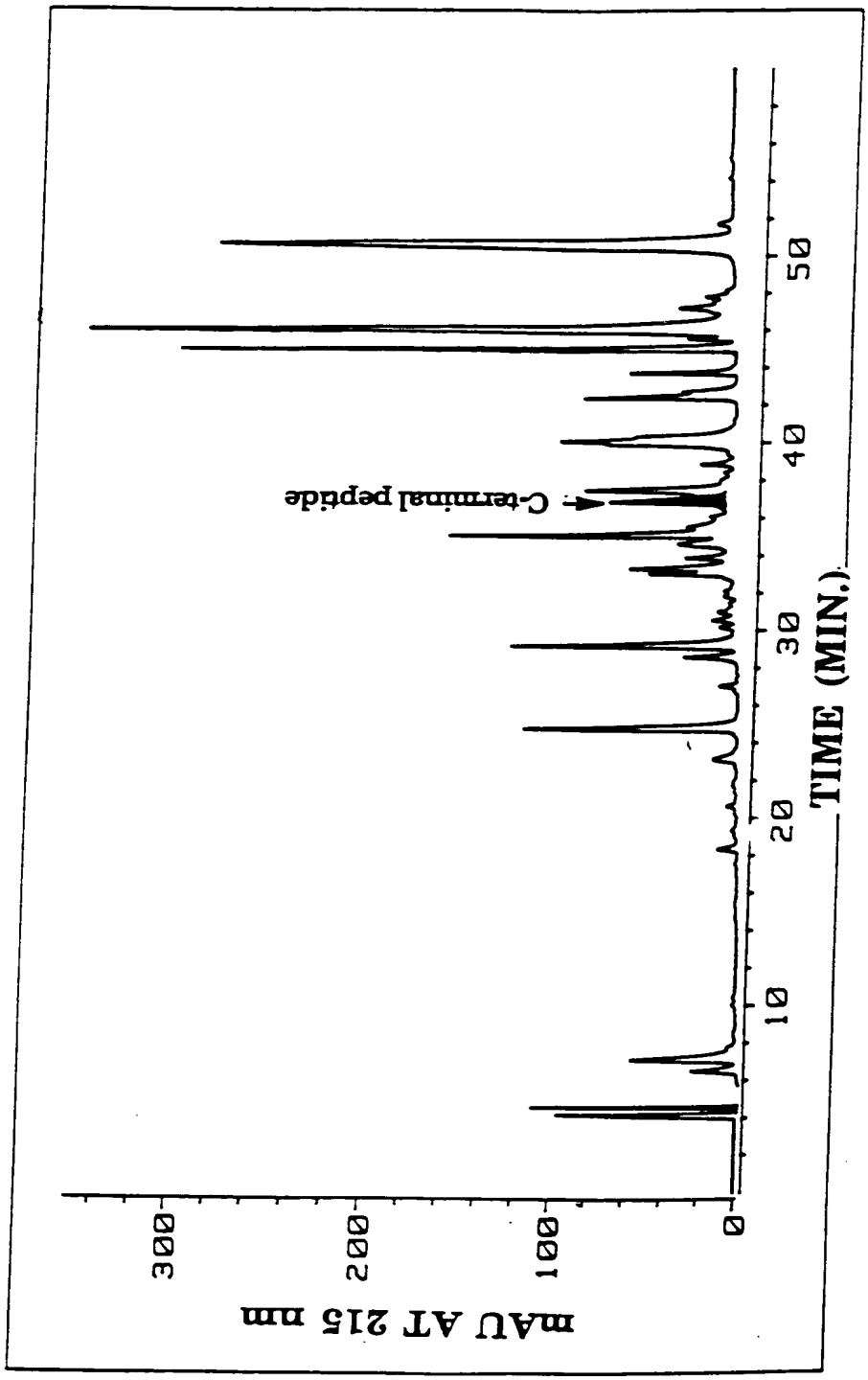

mAU AT 215 nm
300
200
100
0
10
20
30
40
50
TIME (MIN.)
C-terminal peptide

FIG. 16D

EcoRI

```
          ta a t  t  ta a     t  t  c     g     t  a
GAATTCTTCCGTATCTTCAACCGTTCCATCGACGCTTTCAAAGACTTCGTT
E  F  F  R  I  F  N  R  S  I  D  A  F  K  D  F  V

  g  a  t     tagt  t  t  g     t  a  at a ag  t  g
GTTGCTTCCGAAACCTCCGACTGCGTTGTTTCCTCCACCCTGTCTCCGGAA
V  A  S  E  T  S  D  C  V  V  S  S  T  L  S  P  E
```

BstEII

```
      t  a a  ca gt  c  a     a  t  t a  c  t  .  a
AAAGACTCCCGTGTTTCGGTTACCAAACCGTTCATGCTGCCGCCGGTTGCT
K  D  S  R  V  S  V  T  K  P  F  M  L  P  P  V  A

  c ag       t a g  t    ag  ag t ag  ag t   tag t  g     a  t
GCTTCCTCCCTGCGTAACGACTCCTCCTCCTCCAACTCCAAATACATCTAC
A  S  S  L  R  N  D  S  S  S  S  N  S  K  Y  I  Y
```

BamHI

```
     t
CTGATCTAATAGGATCC
L  I  •  •
```

FIG 16E

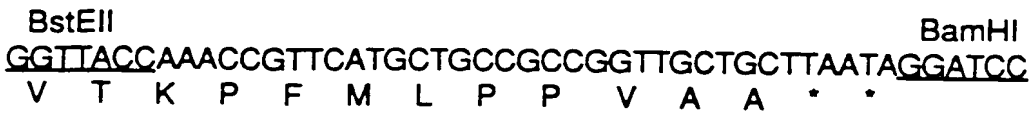
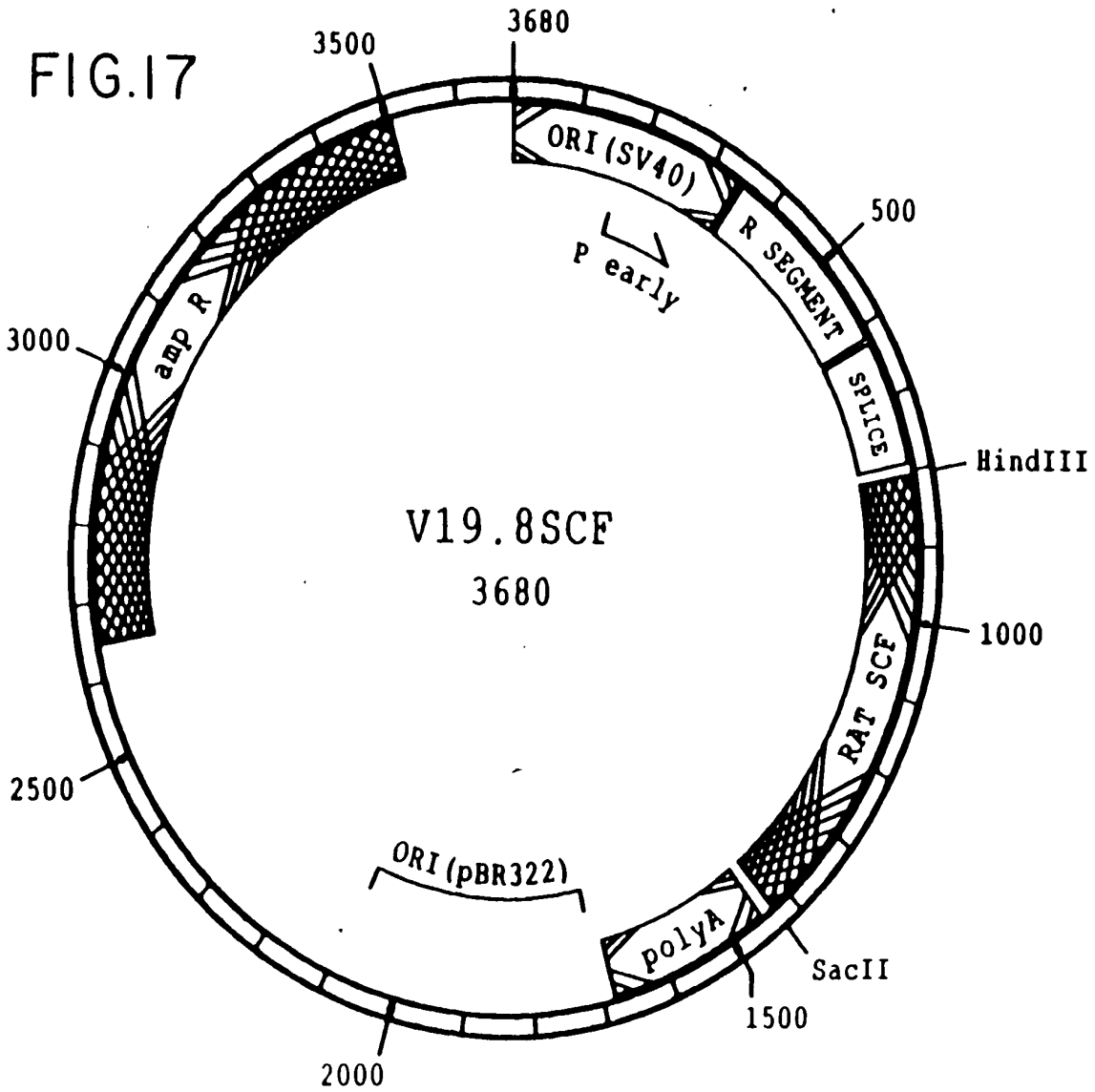

BstEII
BamHI
GGTTACCAAACCGTTCATGCTGCCGCCGGTTGCTGCTTAATAGGATCC
V T K P F M L P P V A A * *

FIG.17


3680
3500
ORI (SV40)
500
P early
R SEGMENT
SPLICE
HindIII
3000
amp R
V19.8SCF
3680
1000
RAT SCF
2500
ORI (pBR322)
polyA
SacII
1500
2000

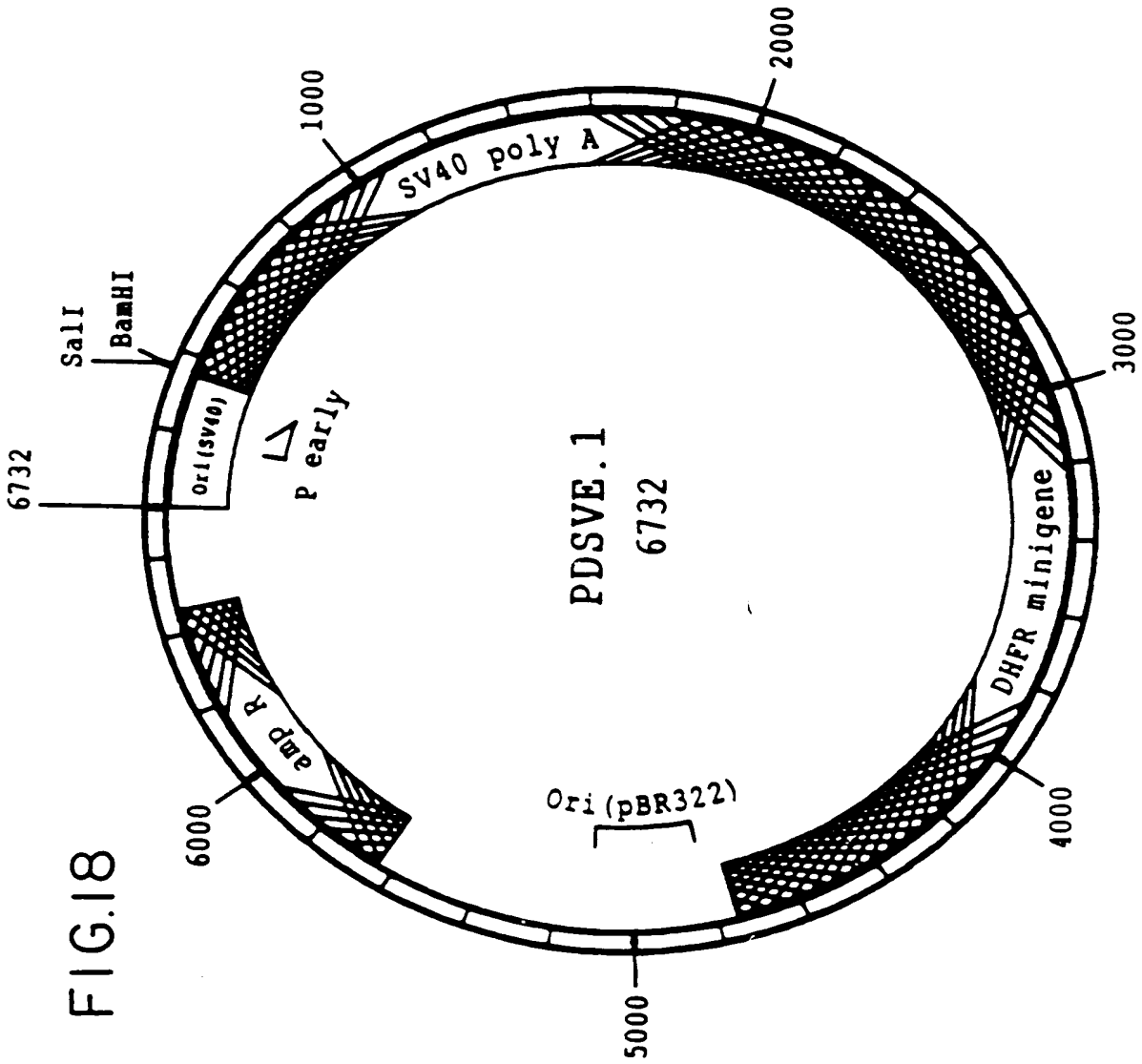

1000
2000
3000
4000
5000
6000
6732
SV40 poly A
SalI
BamHI
Ori(SV40)
P early
PDSVE.1
6732
DHFR minigene
amp R
Ori(pBR322)

FIG.18

FIG.19

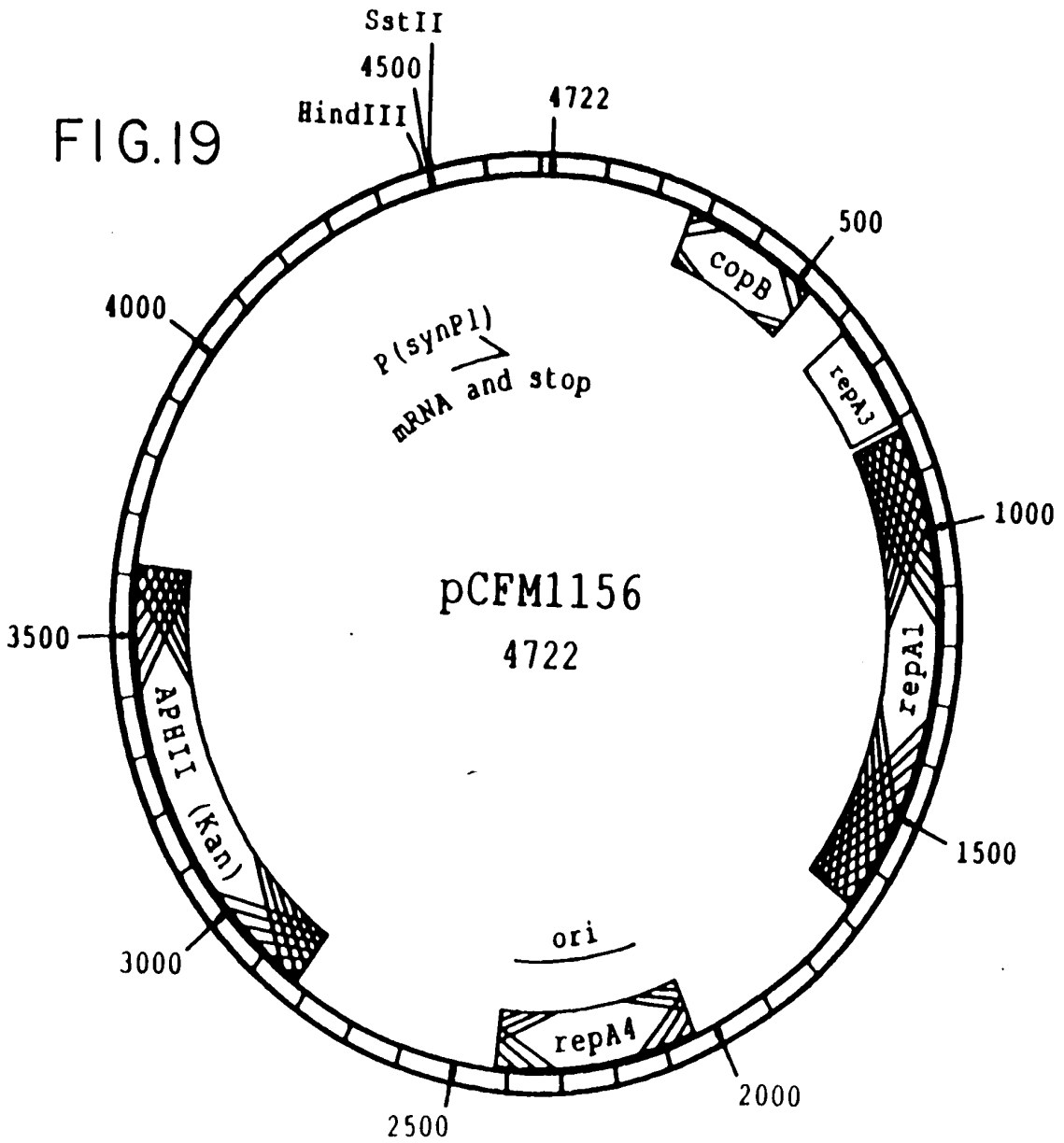

SstII
4500
HindIII
4722
500
1000
1500
2000
2500
3000
3500
4000
copB
repA3
repA1
repA4
APHII (Kan)
P(synPl)
mRNA and stop
ori
pCFM1156
4722

FIG.20A

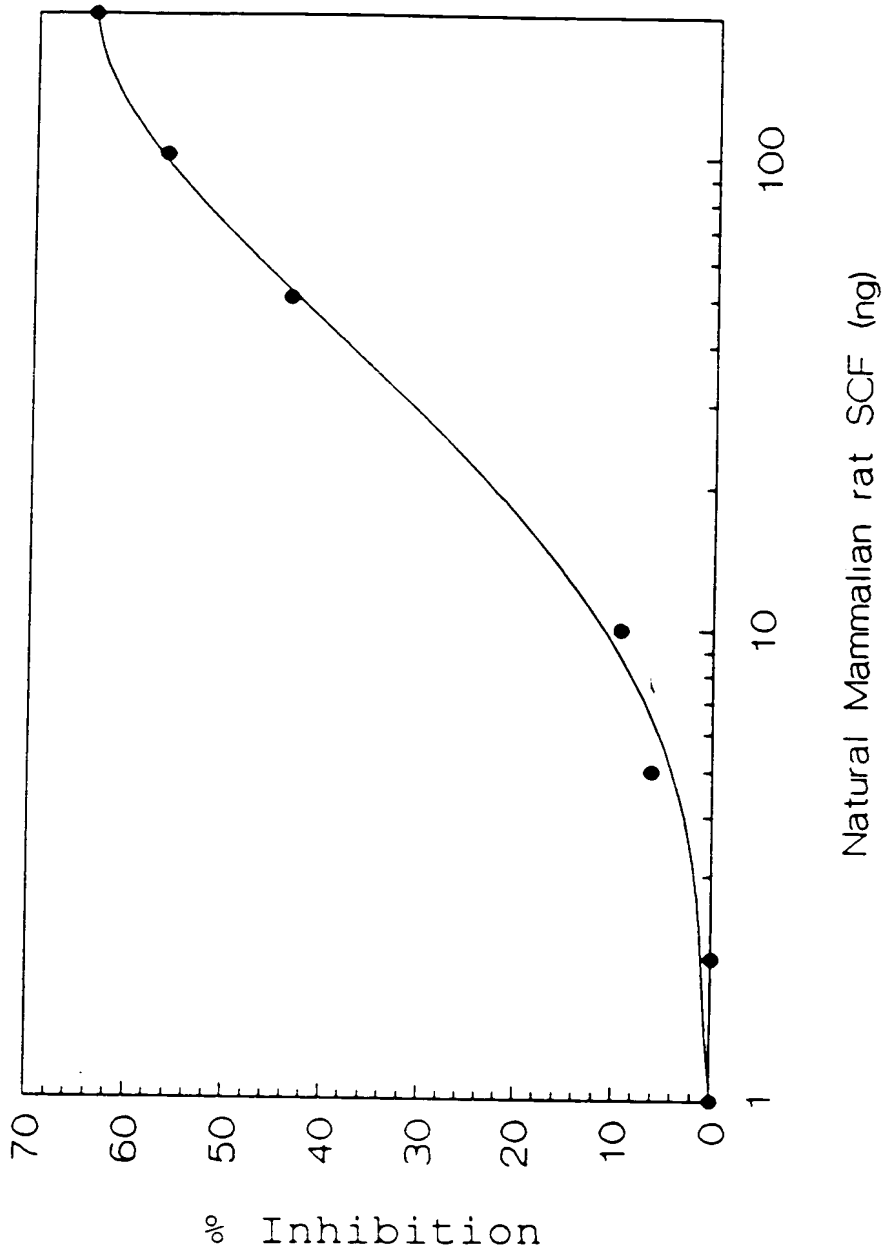

70
60
50
40
30
20
10
0
% Inhibition
1
10
100
Natural Mammalian rat SCF (ng)

FIG.20B



FIG. 21

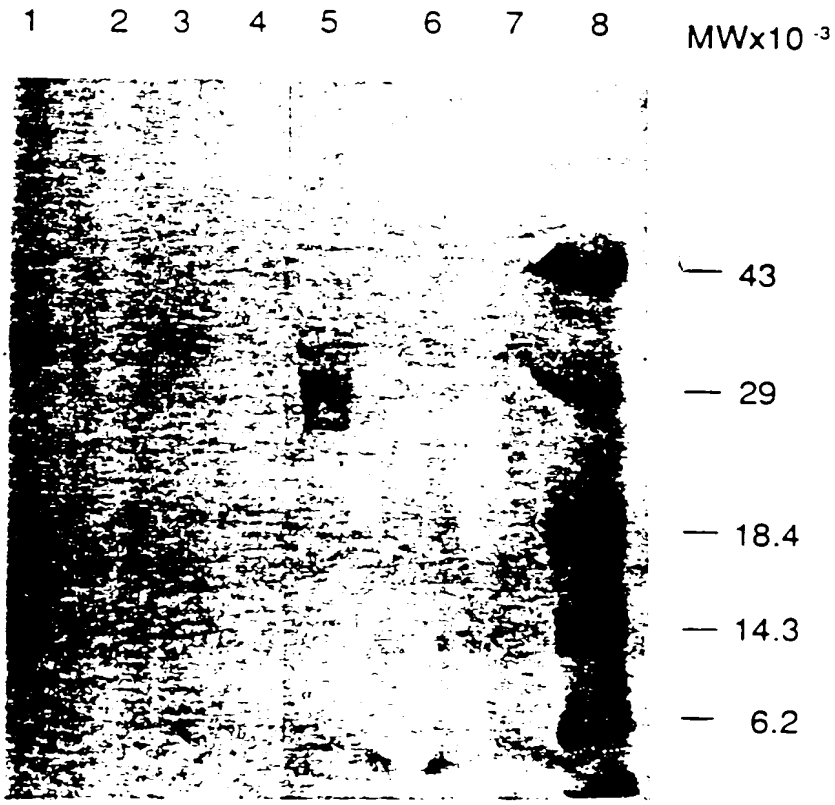


FIG.22

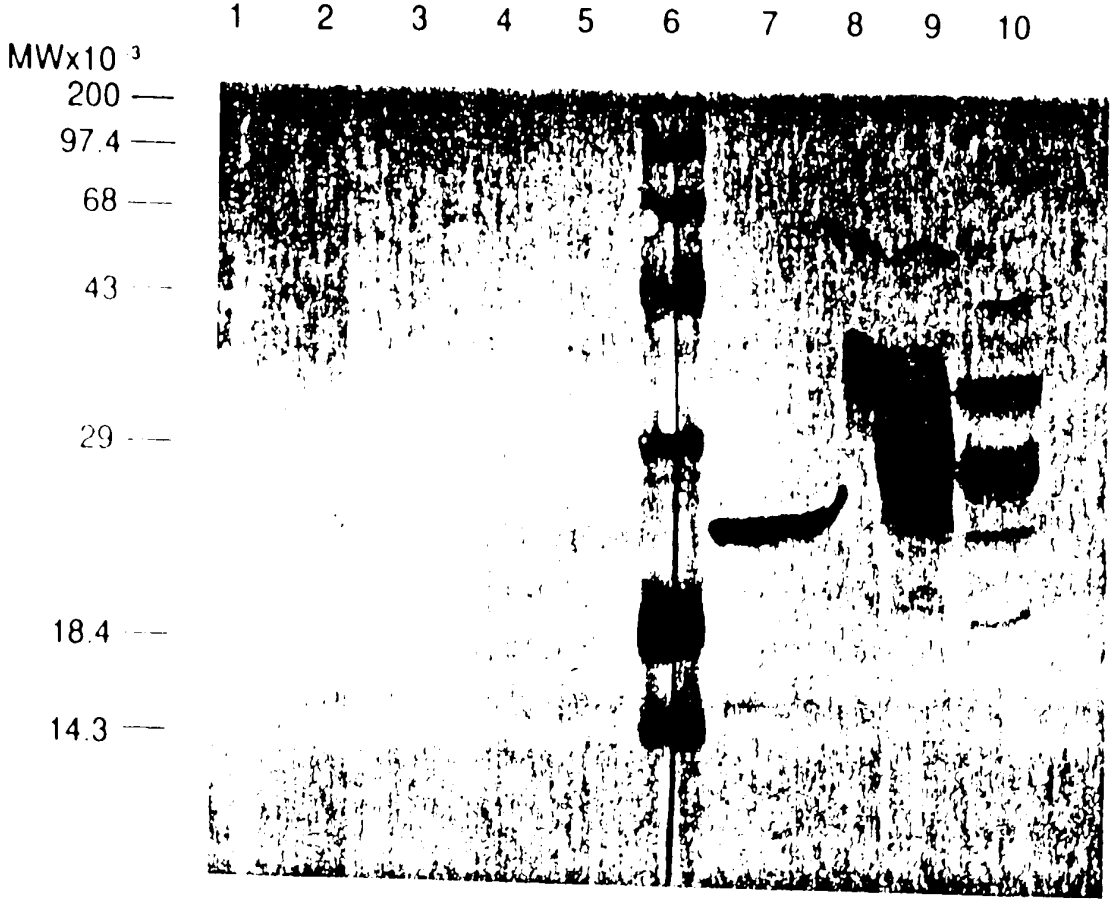


FIG. 22A

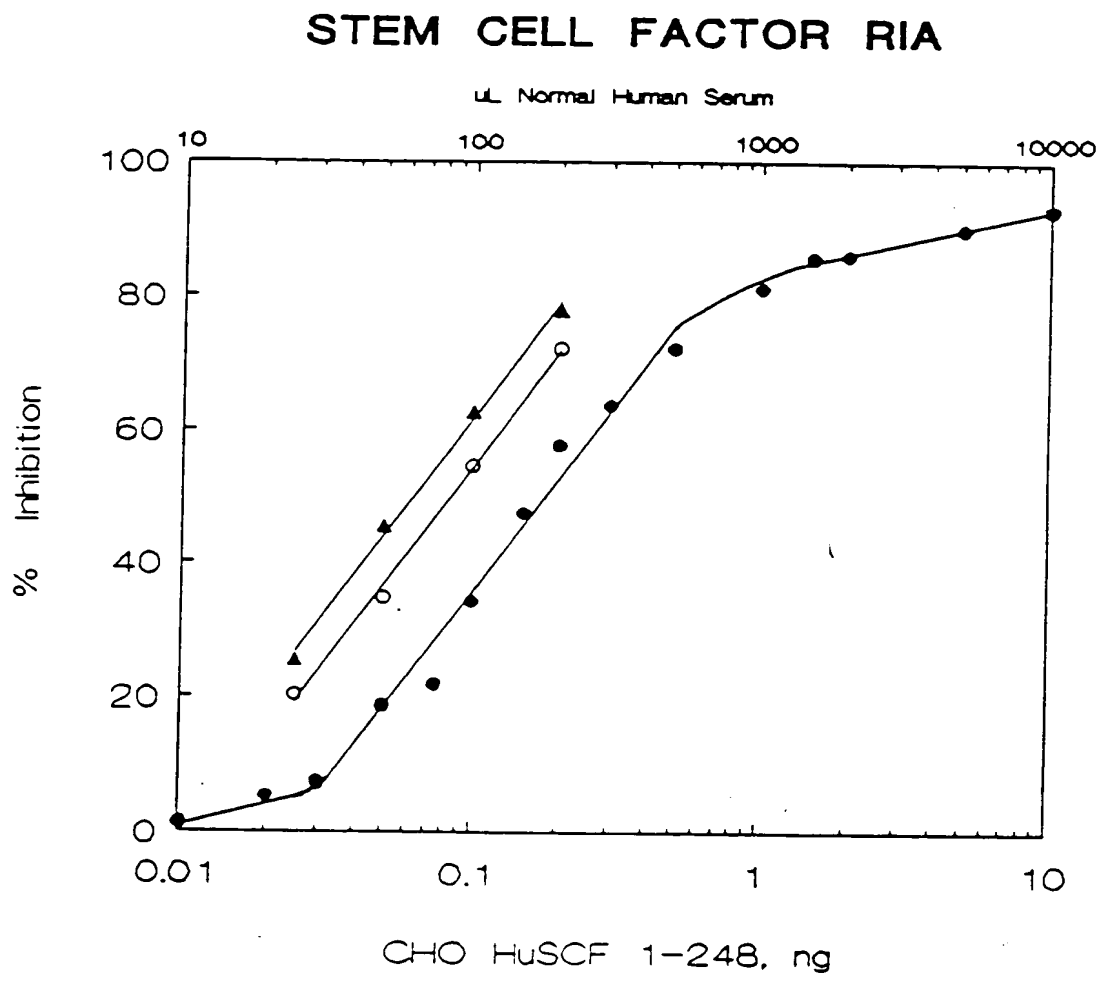

STEM CELL FACTOR RIA
uL Normal Human Serum
10
100
1000
10000
100
80
60
40
20
0
% Inhibition
0.01
0.1
1
10
CHO HuSCF 1-248, ng

FIG. 23

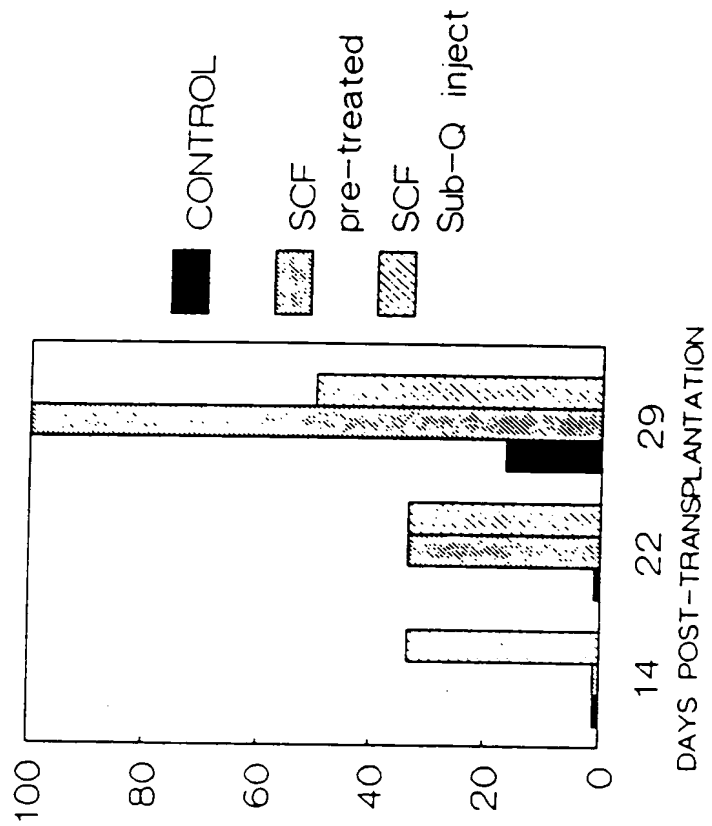

CONTROL
SCF pre-treated
SCF Sub-Q inject
100
80
60
40
20
0
14
22
29
DAYS POST-TRANSPLANTATION
% MICE CONVERTED TO DONOR PHENOTYPE

FIG. 24A

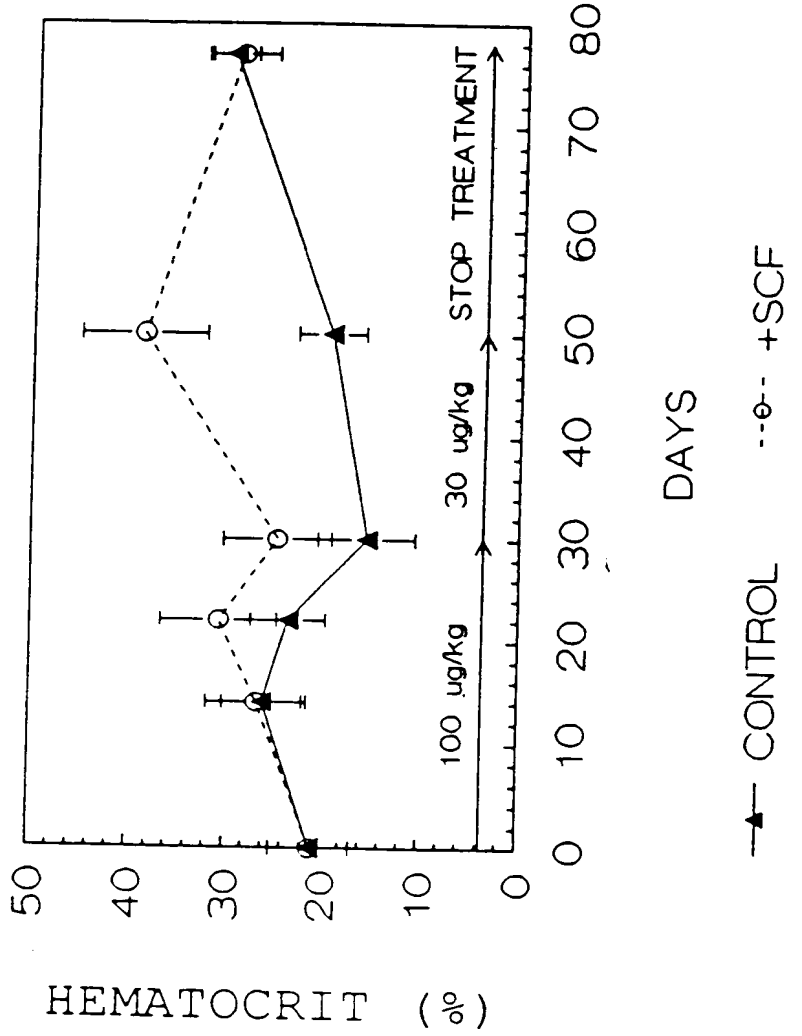

HEMATOCRIT (%)
50
40
30
20
10
0
0
10
20
30
40
50
60
70
80
DAYS
100 µg/kg
30 µg/kg
STOP TREATMENT
CONTROL
+SCF

FIG. 24B

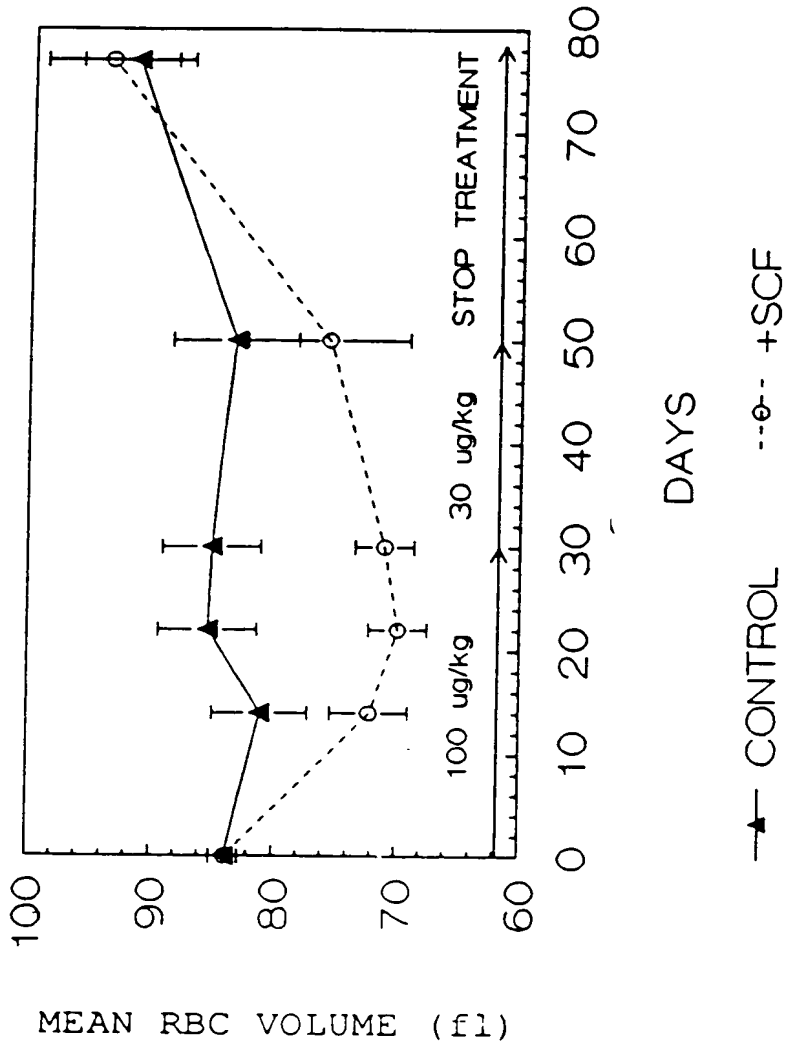

100
90
80
70
60
0
10
20
30
40
50
60
70
80
DAYS
MEAN RBC VOLUME (fl)
100 ug/kg
30 ug/kg
STOP TREATMENT
CONTROL
+SCF

FIG. 25

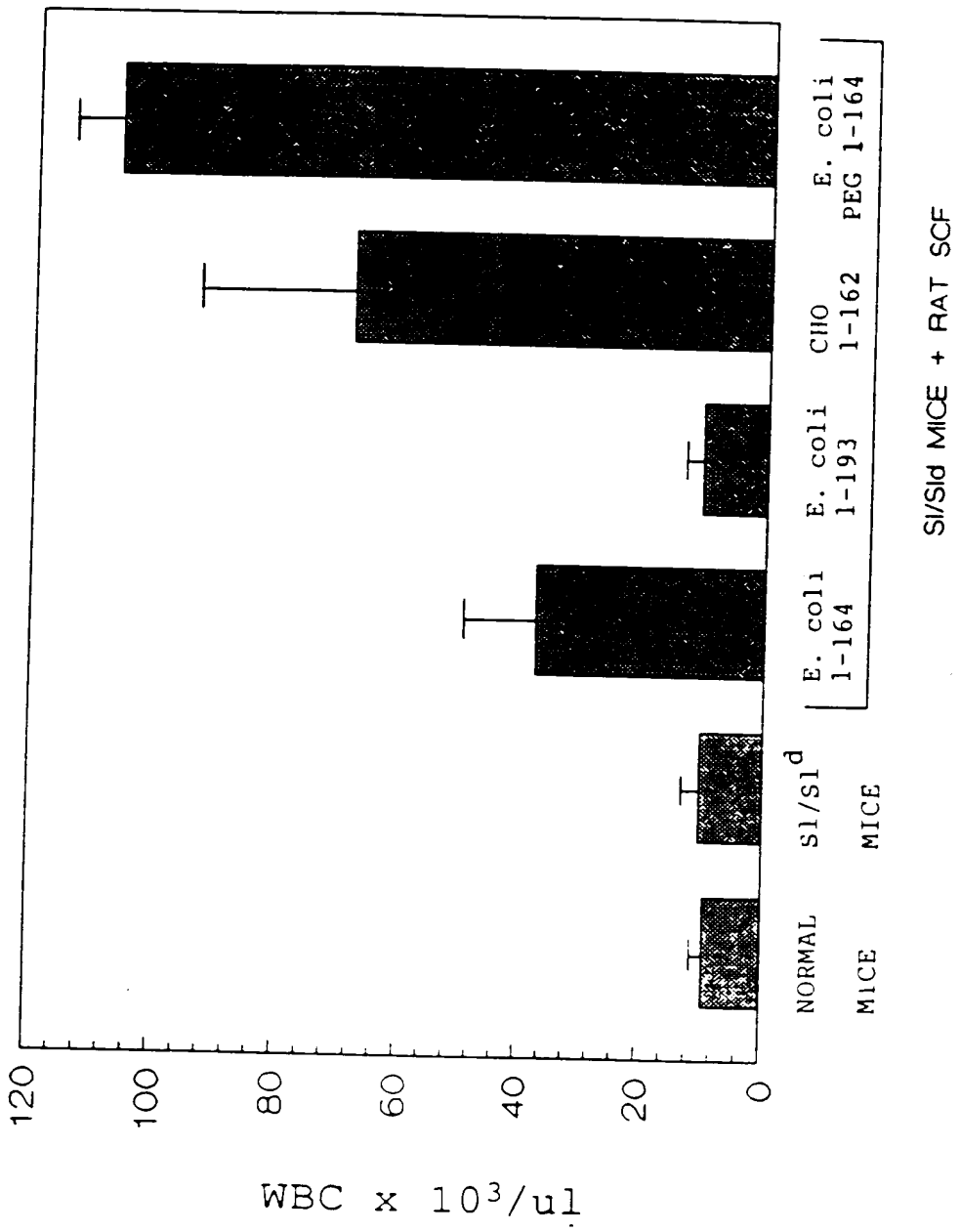

120
100
80
60
40
20
0
WBC x 10^3/ul
NORMAL MICE
Sl/Sl^d MICE
E. coli 1-164
E. coli 1-193
CHO 1-162
E. coli PEG 1-164
Sl/Sld MICE + RAT SCF

FIG. 26

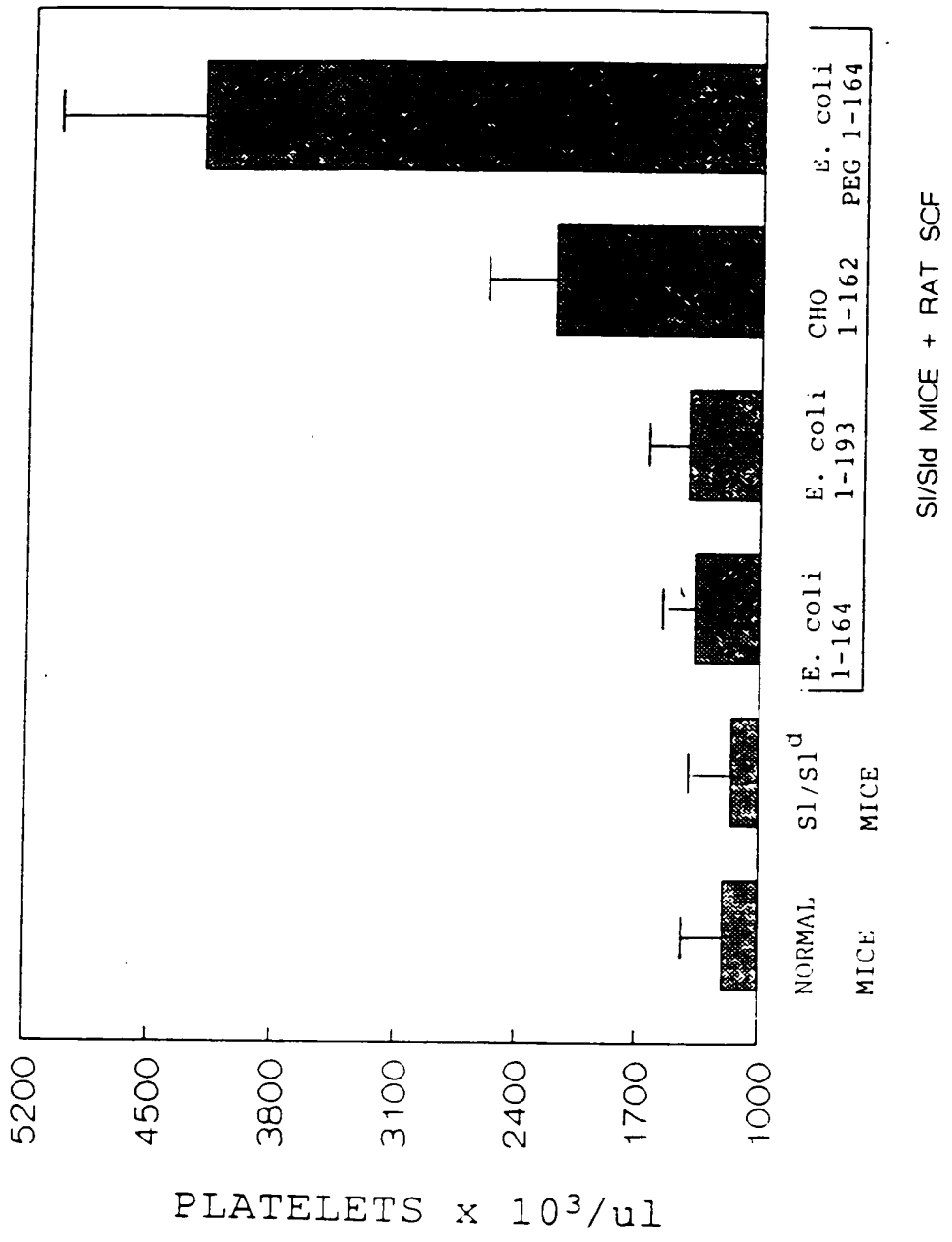

5200
4500
3800
3100
2400
1700
1000
PLATELETS x 10^3/ul
NORMAL MICE
Sl/Sl^d MICE
E. coli 1-164
E. coli 1-193
CHO 1-162
E. coli PEG 1-164
Sl/Sld MICE + RAT SCF

FIG. 27

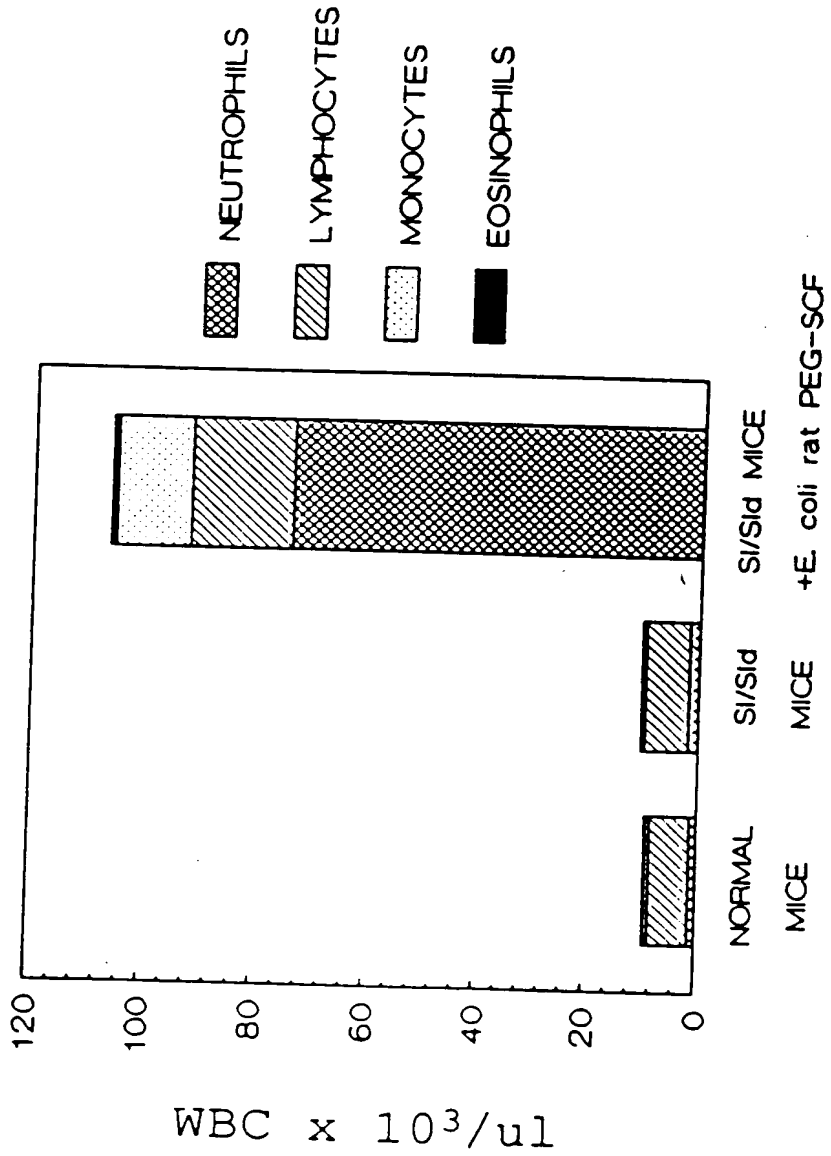

NEUTROPHILS
LYMPHOCYTES
MONOCYTES
EOSINOPHILS
NORMAL MICE
Sl/Sld MICE
Sl/Sld MICE +E. coli rat PEG-SCF
120
100
80
60
40
20
0
WBC x 10³/ul

FIG. 28

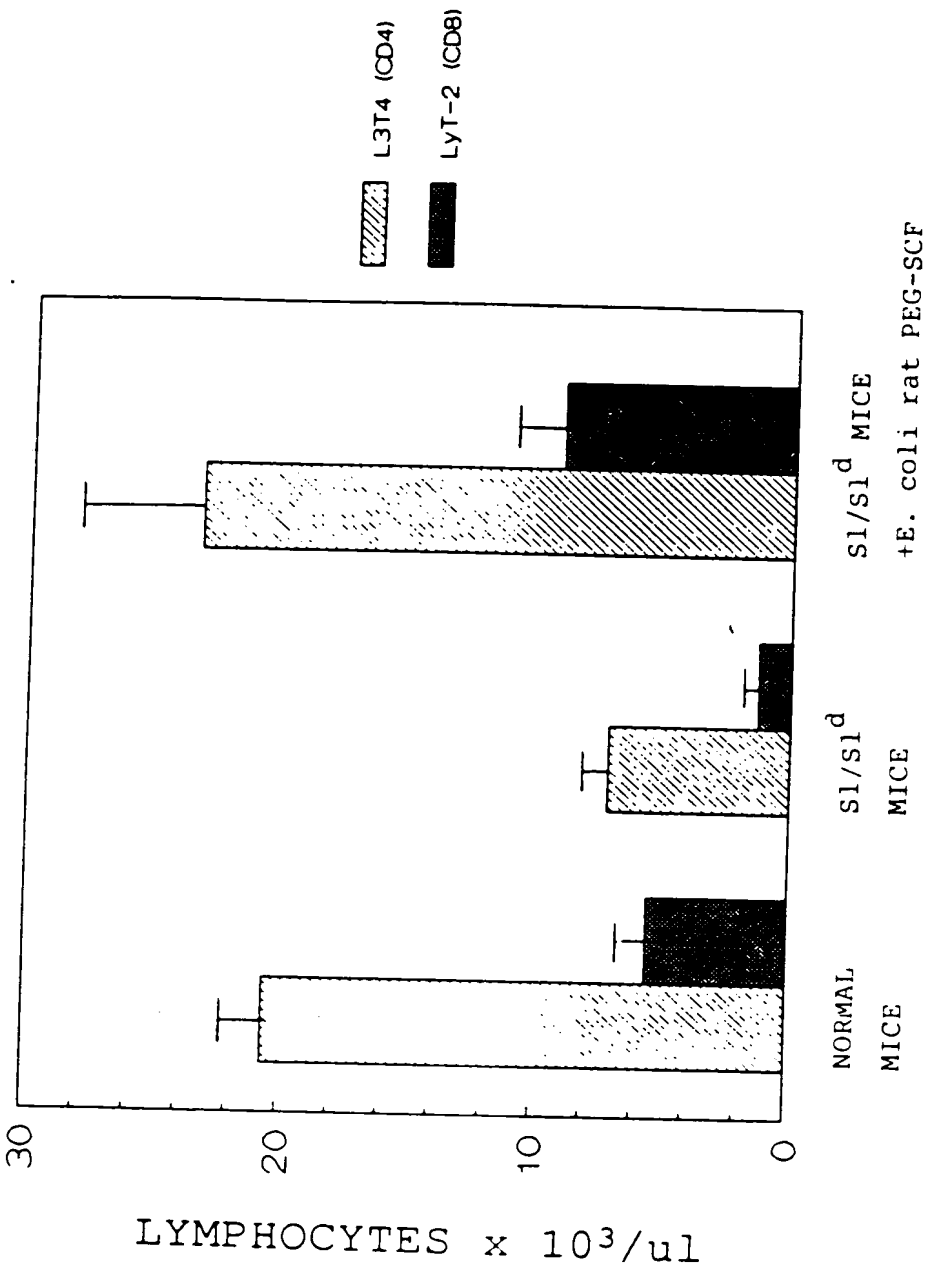

L3T4 (CD4)
LyT-2 (CD8)
30
20
10
0
LYMPHOCYTES x 10³/ul
NORMAL MICE
Sl/Sl^d MICE
Sl/Sl^d MICE +E. coli rat PEG-SCF

FIG.29A

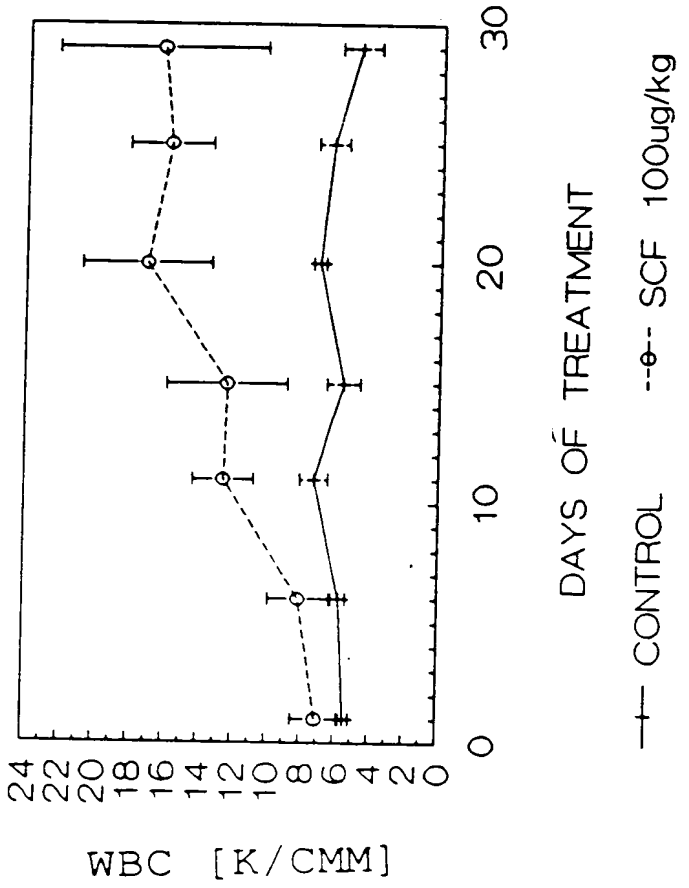

24
22
20
18
16
14
12
10
8
6
4
2
0
WBC [K/CMM]
0
10
20
30
DAYS OF TREATMENT
CONTROL
SCF 100ug/kg

FIG. 29B

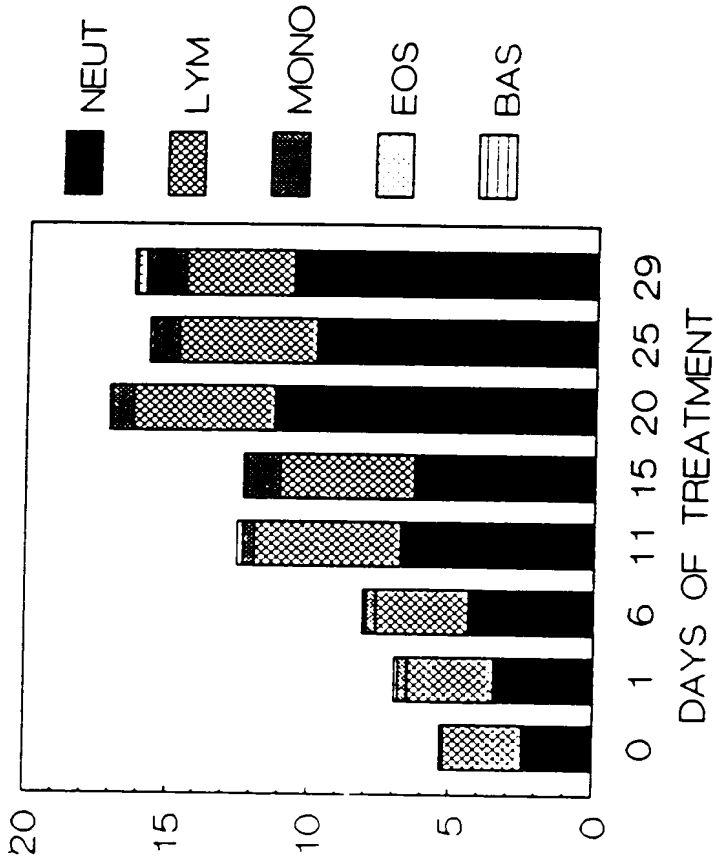

NEUT
LYM
MONO
EOS
BAS
0 1 6 11 15 20 25 29
DAYS OF TREATMENT
20 15 10 5 0
PERIPHERAL BLOOD CELLS [K/CMM]

FIG.30A

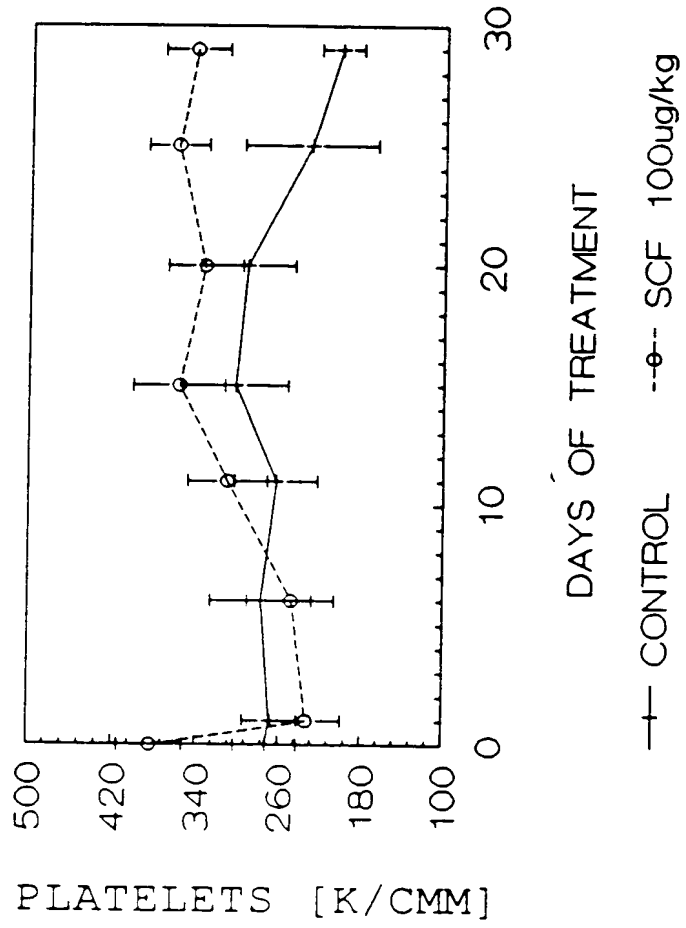

500
420
340
260
180
100
0
10
20
30
PLATELETS [K/CMM]
DAYS OF TREATMENT
CONTROL
SCF 100ug/kg

FIG.30B

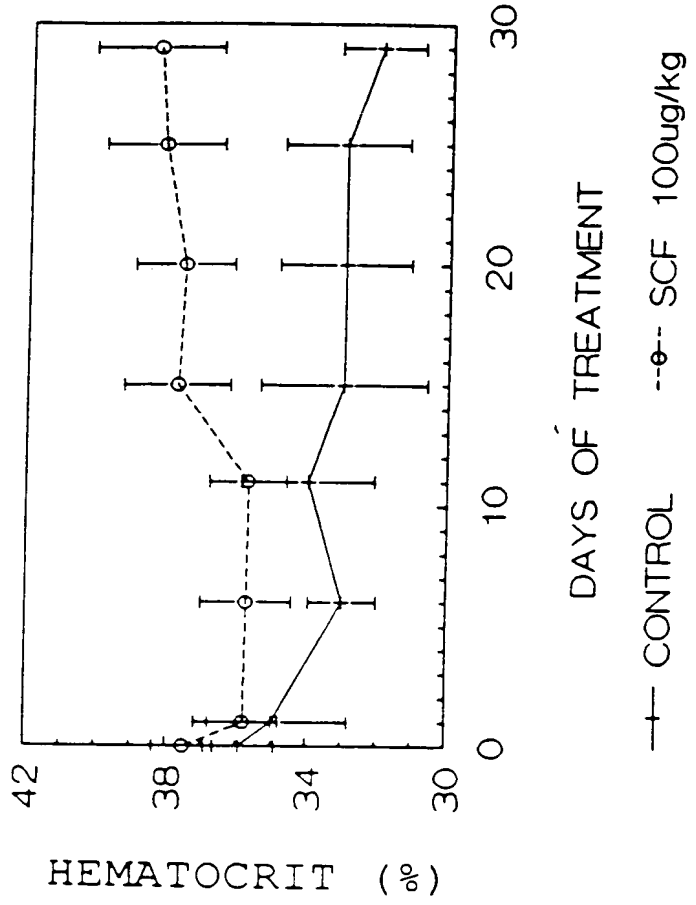

42
38
34
30
HEMATOCRIT (%)
0
10
20
30
DAYS OF TREATMENT
CONTROL
SCF 100ug/kg

FIG. 31A



FIG. 31B

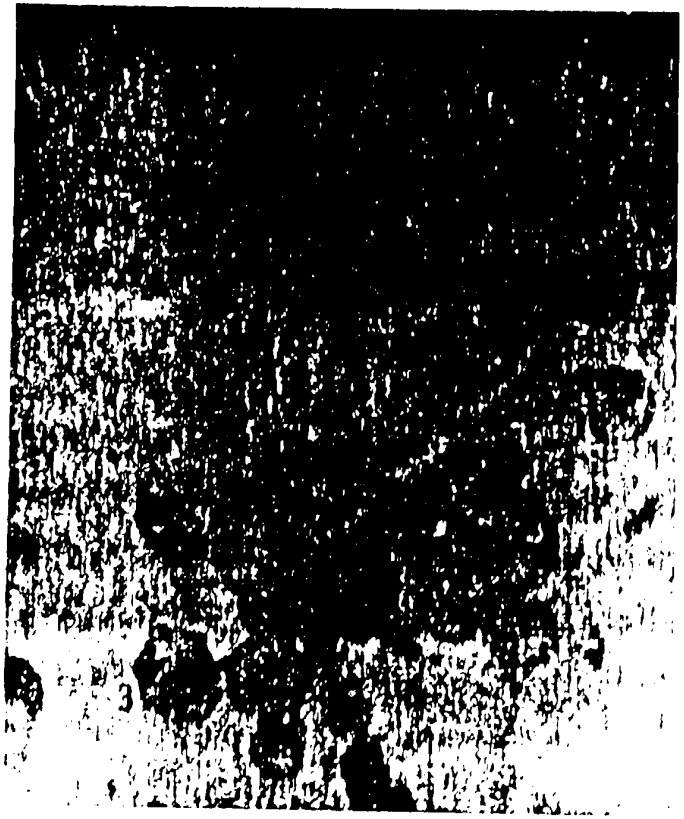


FIG. 31C

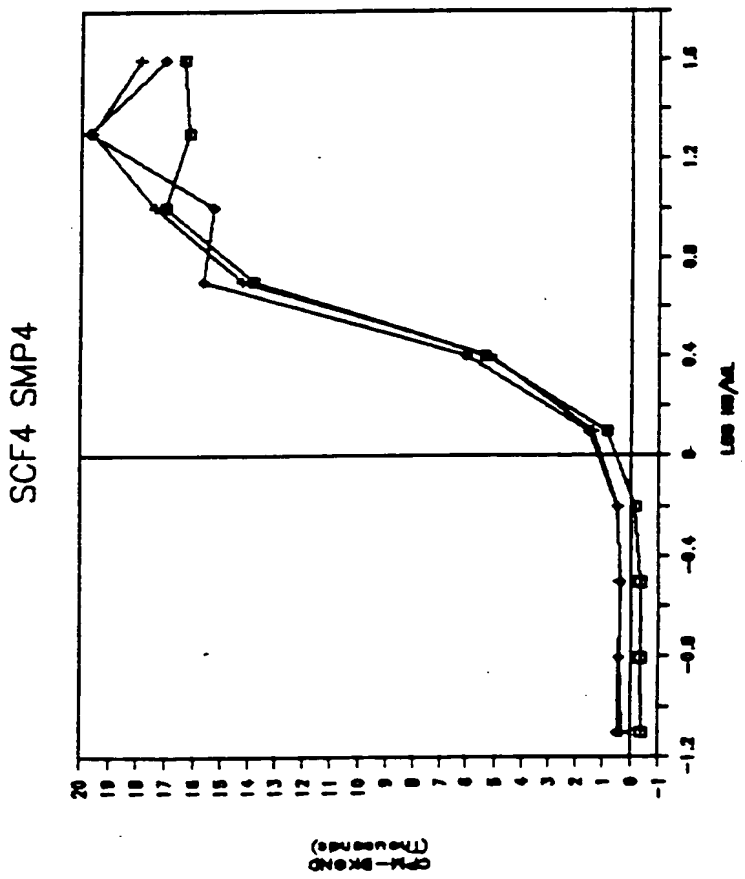


FIG. 32A

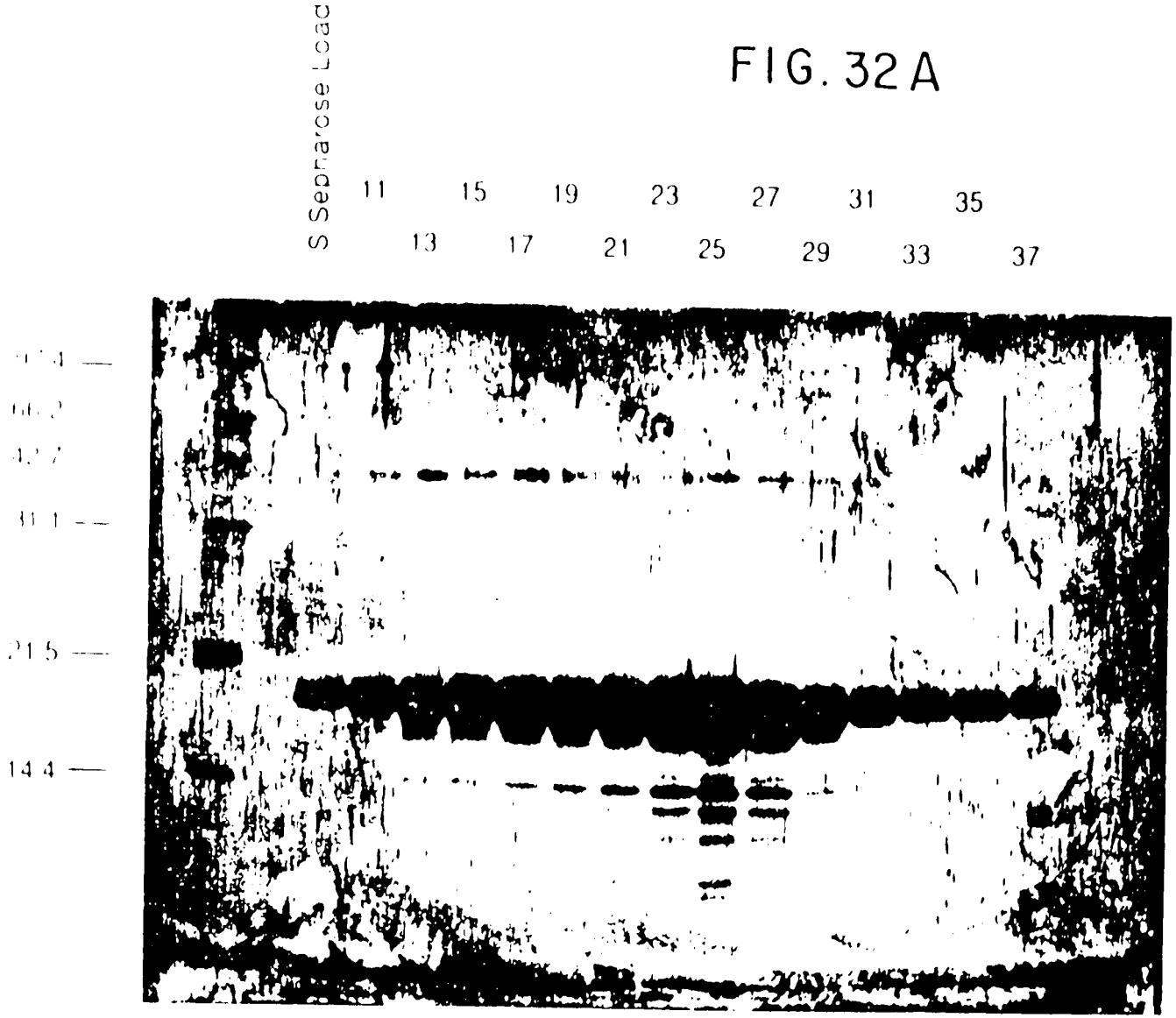


FIG. 32 B

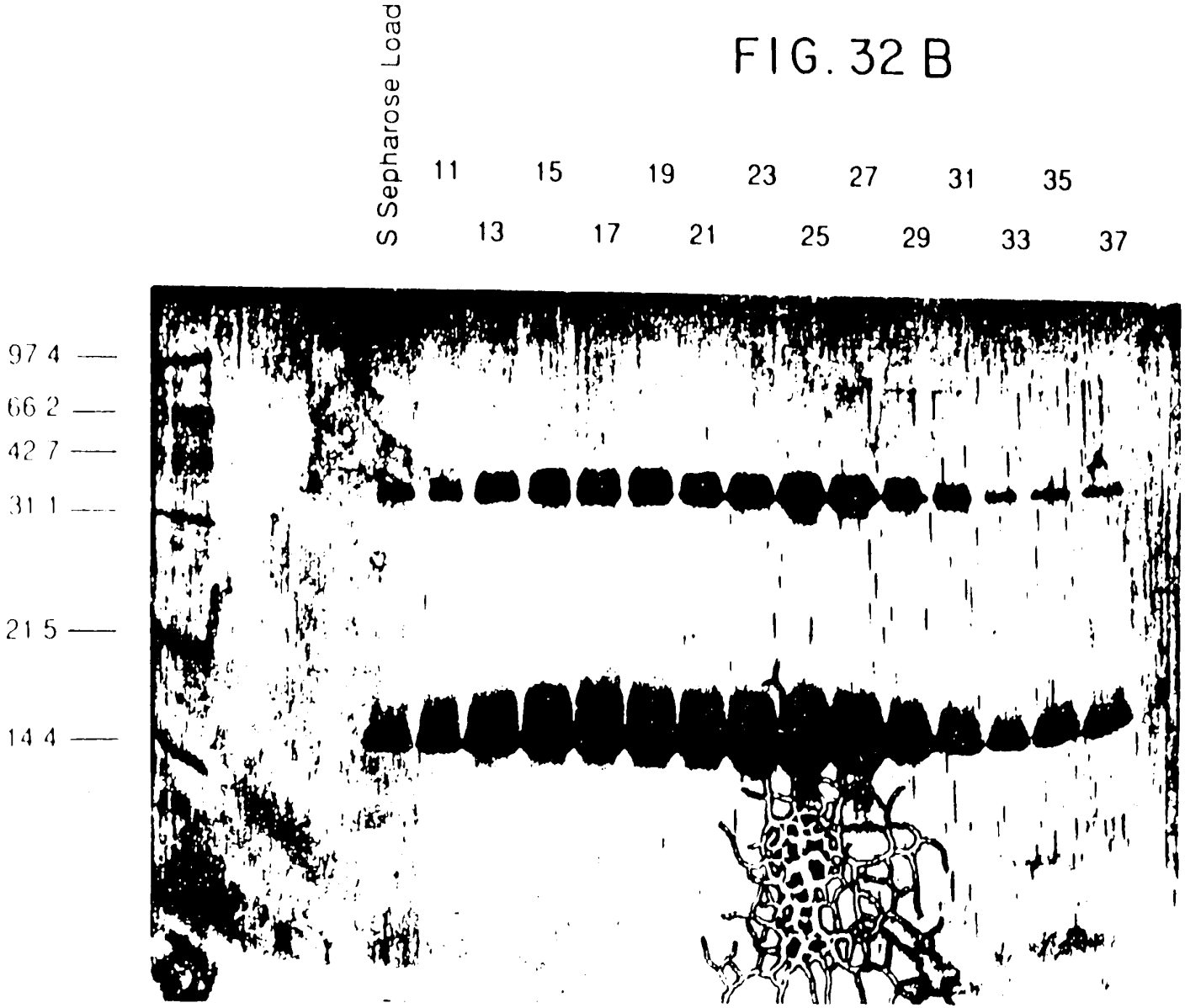

S Sepharose Load
11
13
15
17
19
21
23
25
27
29
31
33
35
37
97 4
66 2
42 7
31 1
21 5
14 4

FIG.33

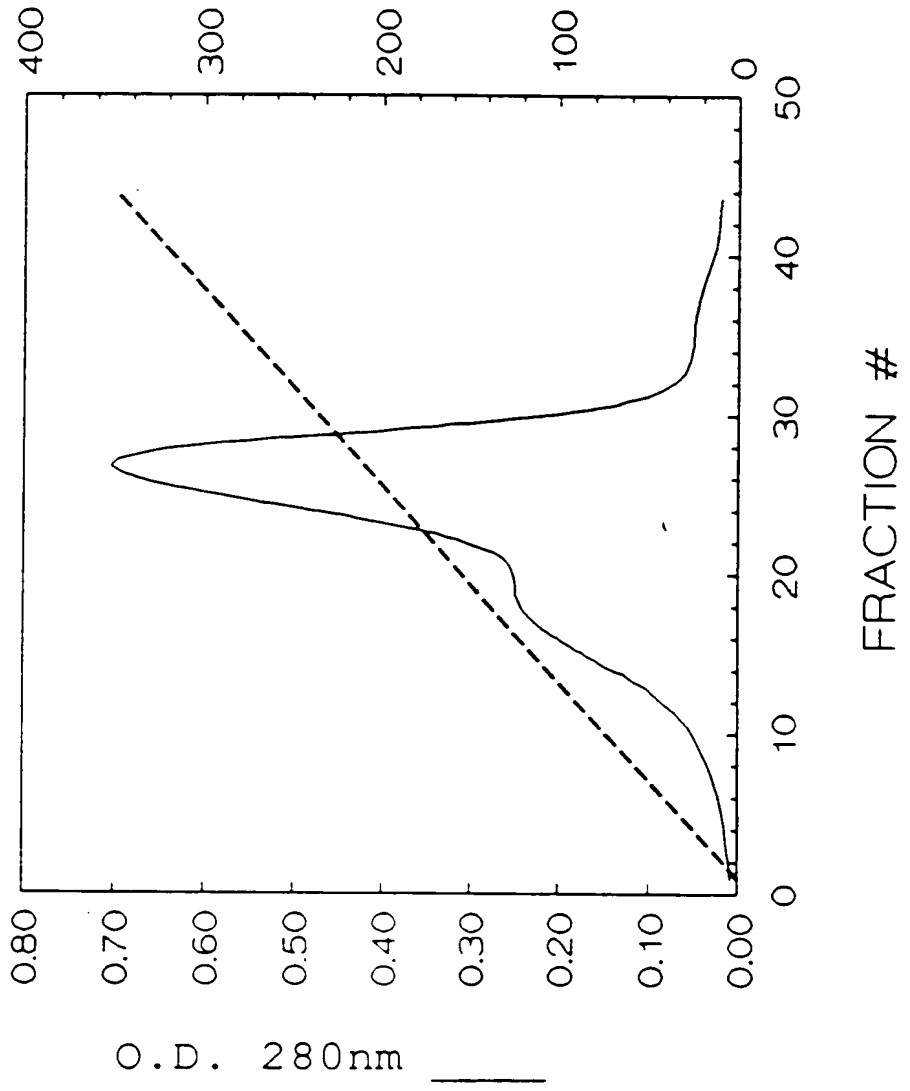

NaCl (mM) -----
400
300
200
100
0
50
40
30
20
10
0
FRACTION #
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
O.D. 280nm ____

FIG.34A

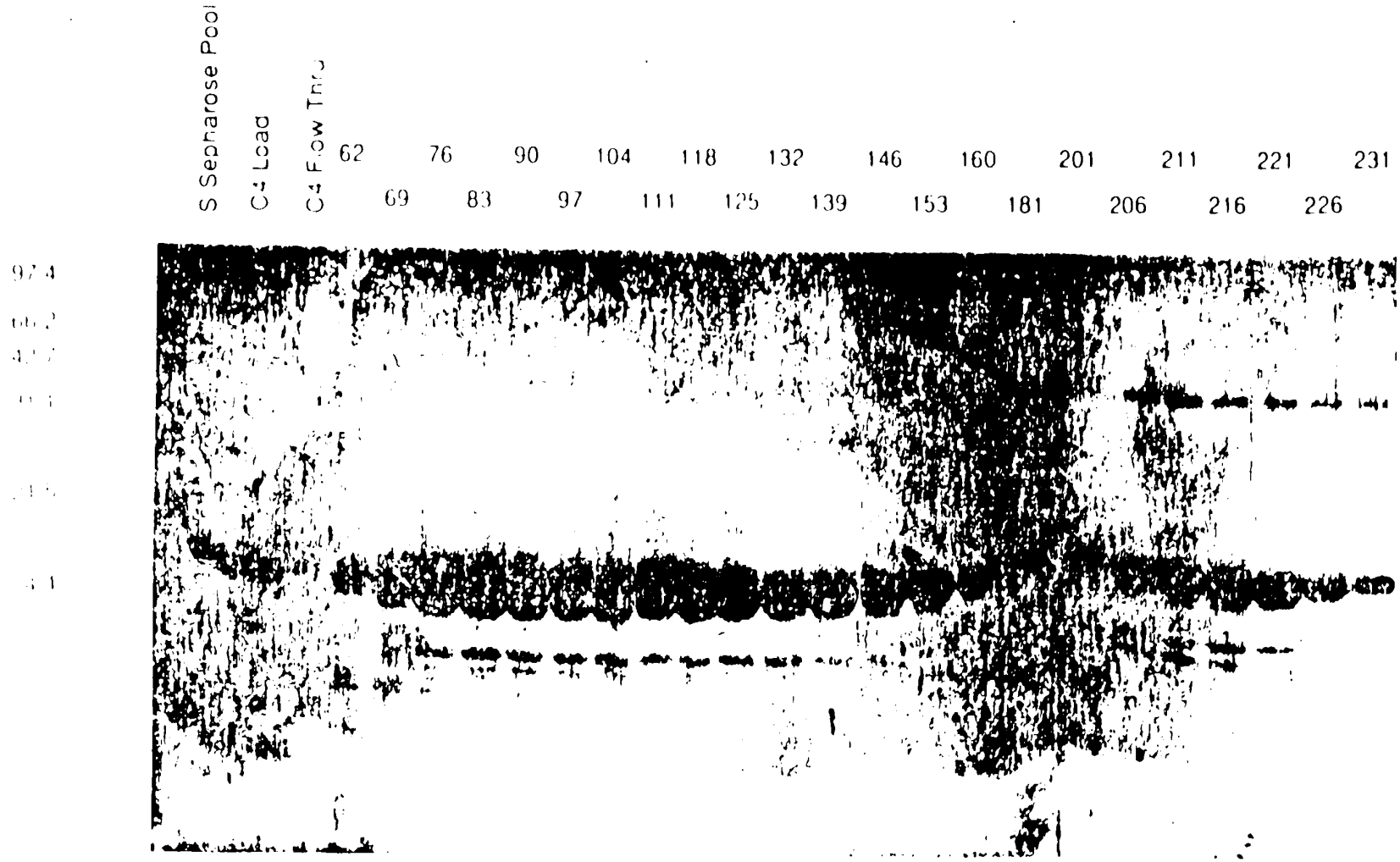

S Sepharose Pool
C4 Load
C4 Flow Thru
62
76
90
104
118
132
146
160
201
211
221
231
69
83
97
111
125
139
153
181
206
216
226

FIG. 34B

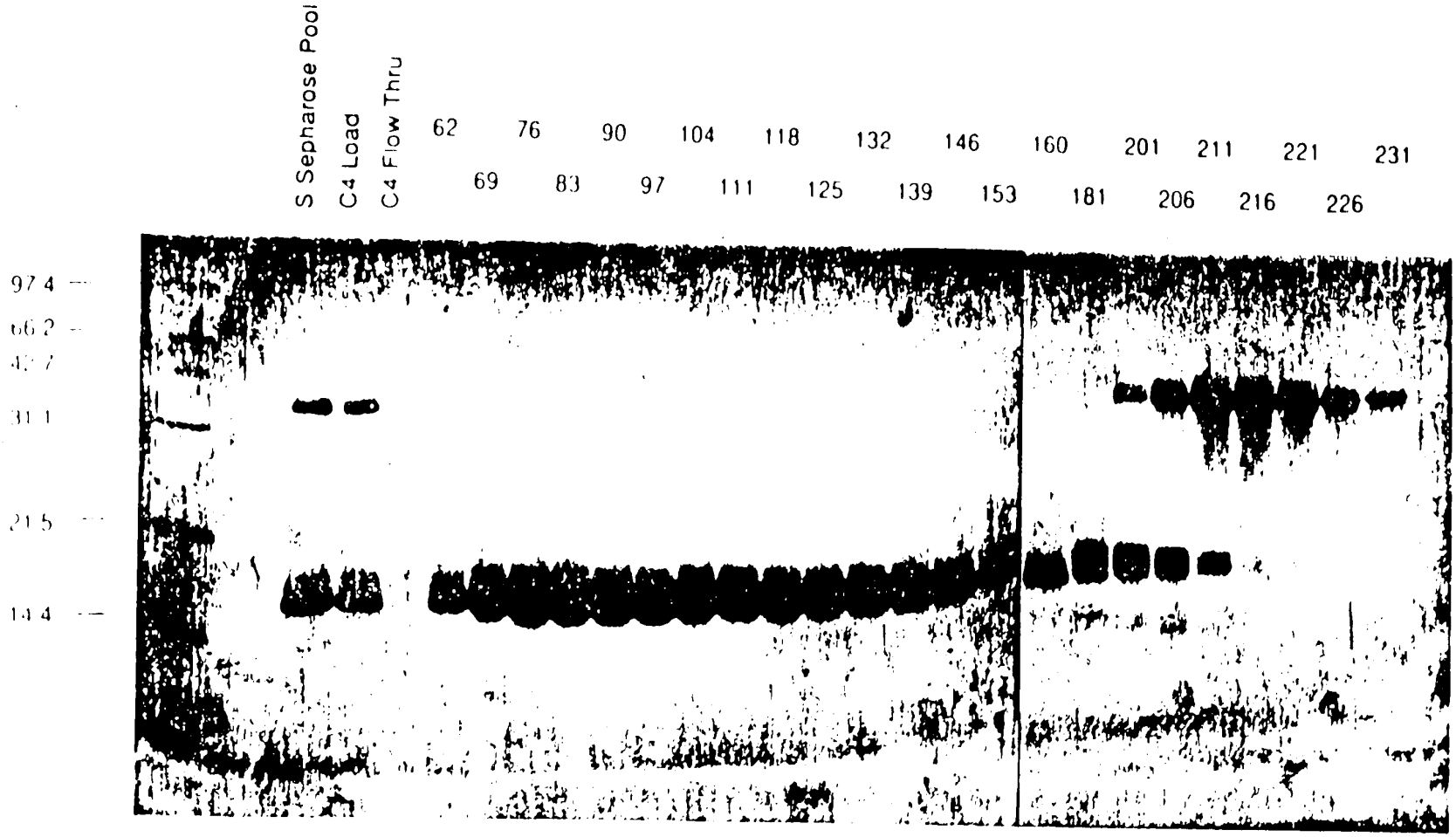

S Sepharose Pool
C4 Load
C4 Flow Thru
62
69
76
83
90
97
104
111
118
125
132
139
146
153
160
181
201
206
211
216
221
226
231
97.4
66.2
43.7
31.1
21.5
14.4

FIG. 35

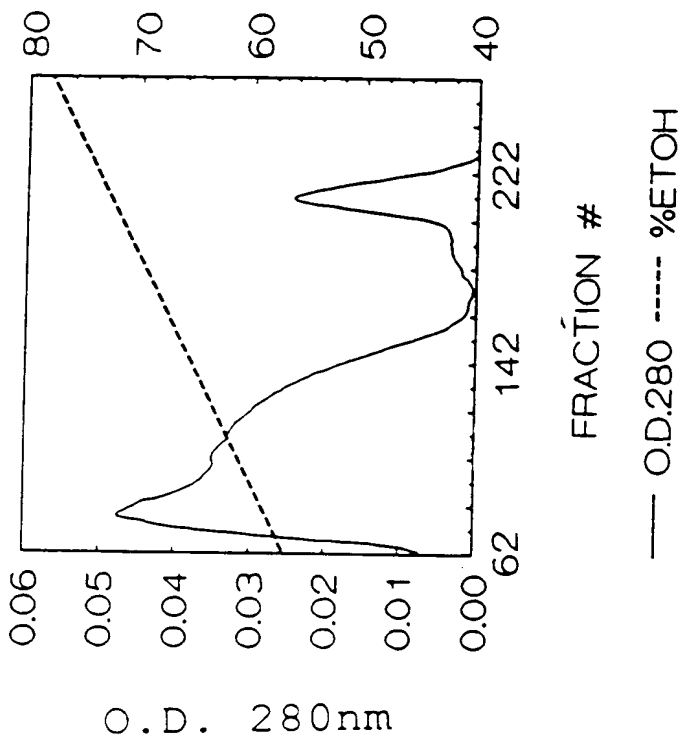

ETHANOL (%)
80
70
60
50
40
222
142
62
FRACTION #
— O.D.280 ----- %ETOH
0.06
0.05
0.04
0.03
0.02
0.01
0.00
O.D. 280nm

FIG. 36

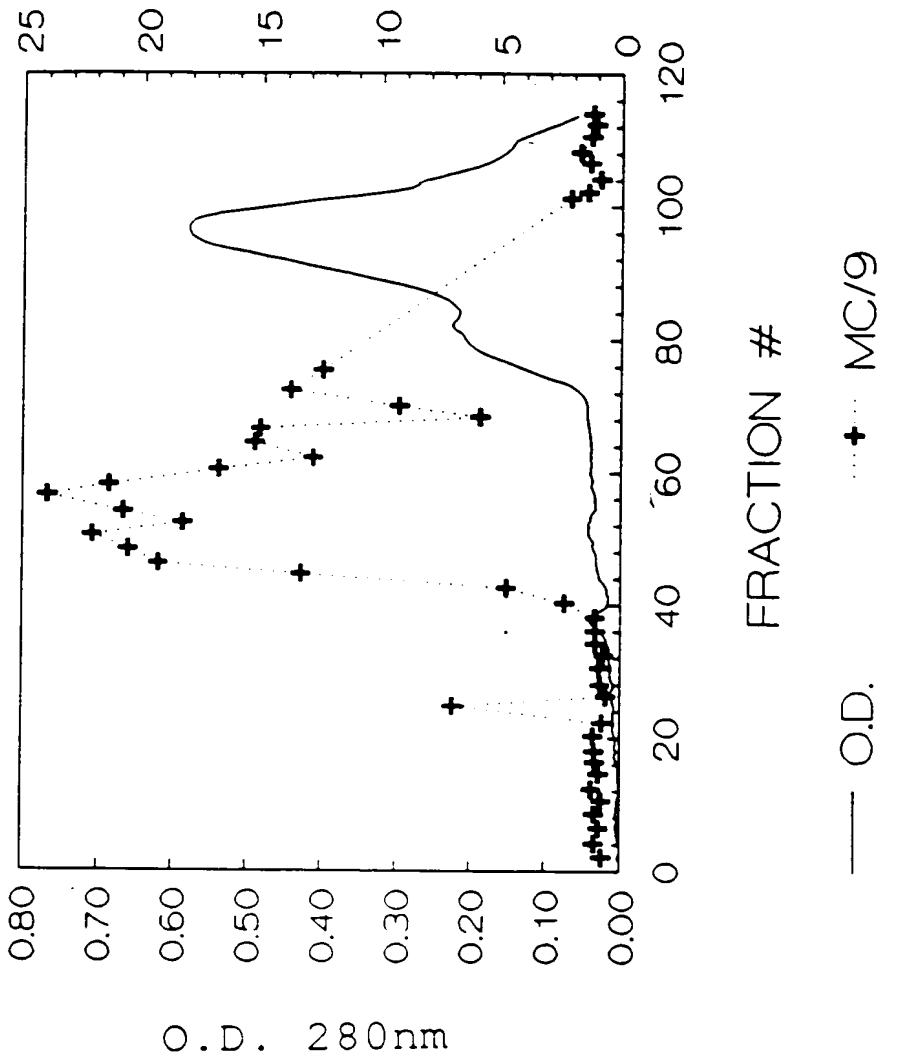

MC/9 CPM (x 10⁻³)
25
20
15
10
5
0
120
100
80
60
40
20
0
FRACTION #
MC/9
O.D.
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
O.D. 280nm

FIG. 37

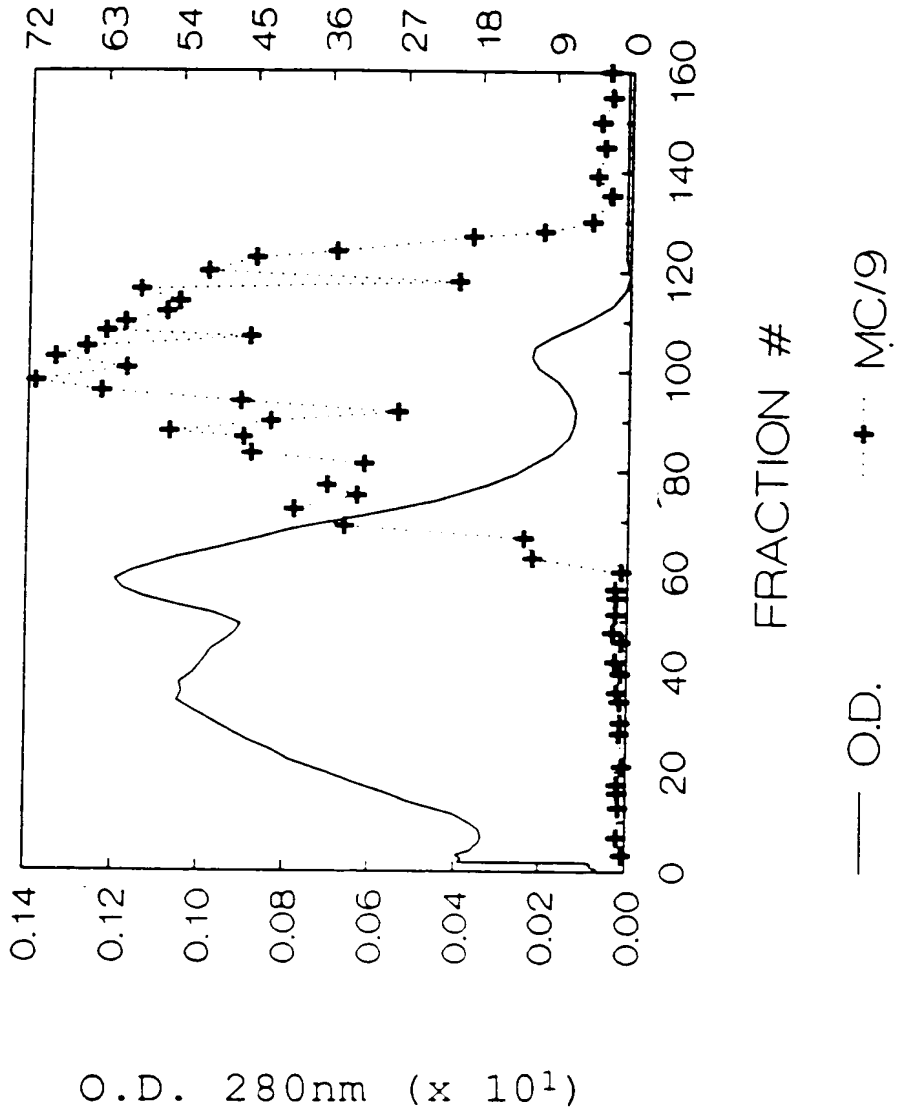

MC/9 CPM (x 10⁻³)
72
63
54
45
36
27
18
9
0
160
140
120
100
80
60
40
20
0
FRACTION #
MC/9
O.D.
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00
O.D. 280nm (x 10¹)

FIG.38

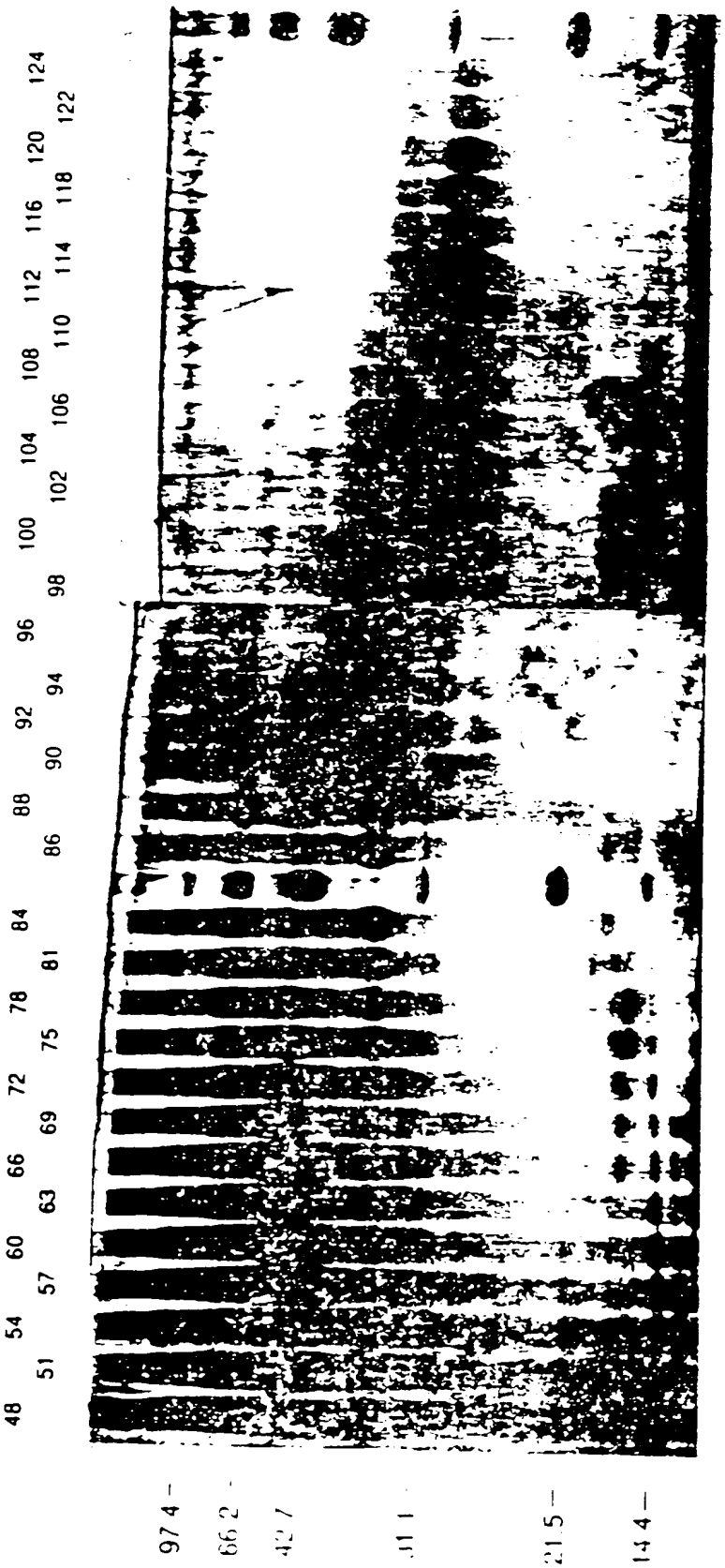

48
51
54
57
60
63
66
69
72
75
78
81
84
86
88
90
92
94
96
98
100
102
104
106
108
110
112
114
116
118
120
122
124
97.4
66.2
42.7
31.1
21.5
14.4

FIG. 39

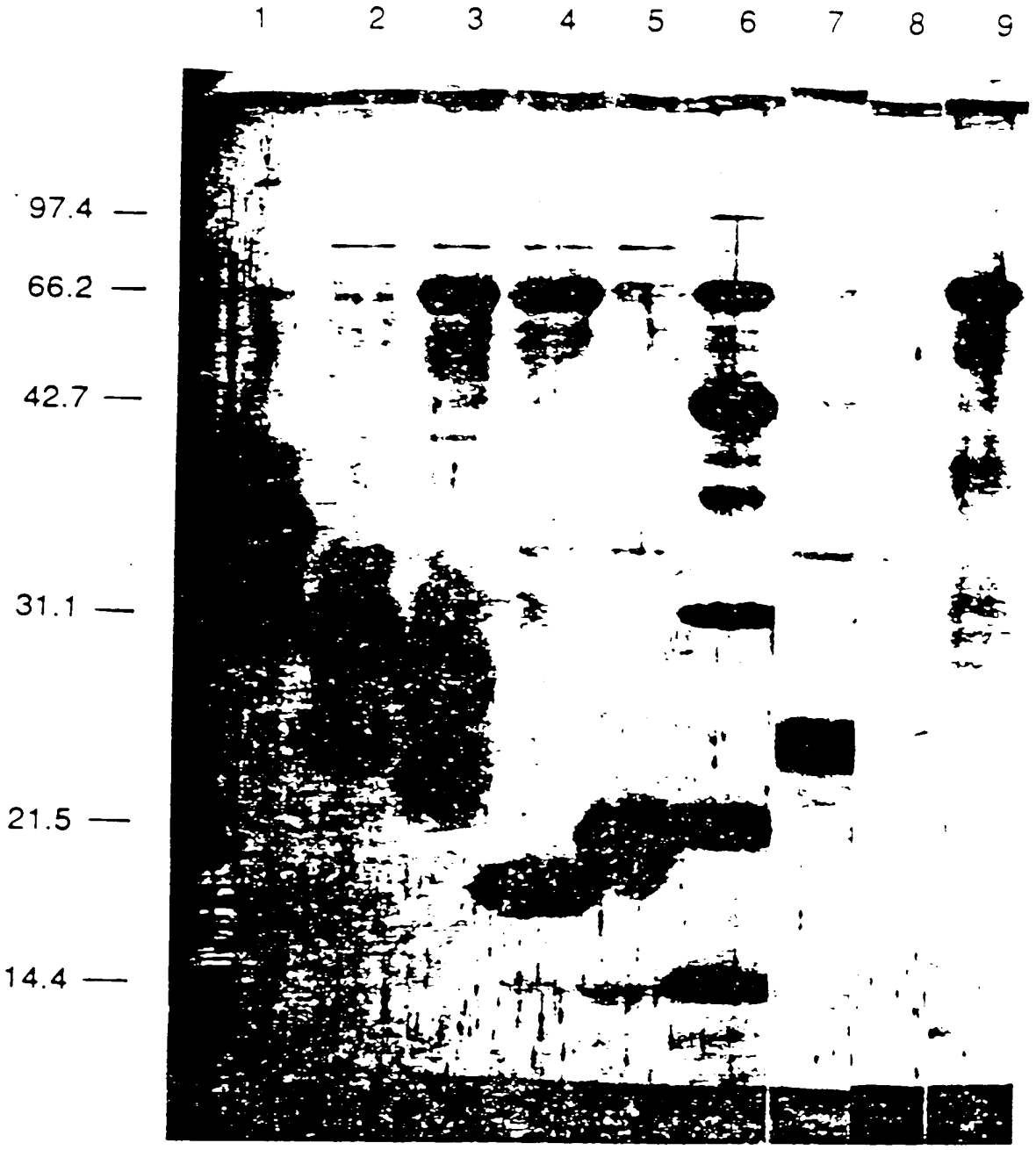


FIG. 40A

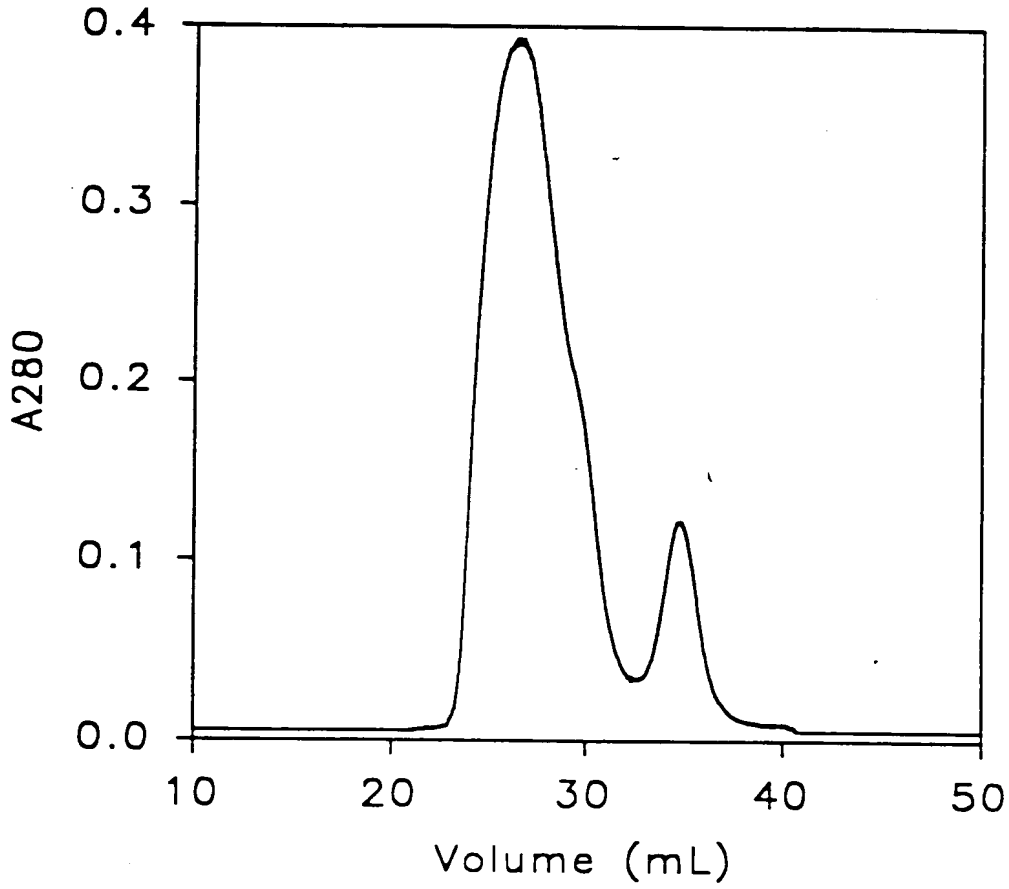


FIG. 40B

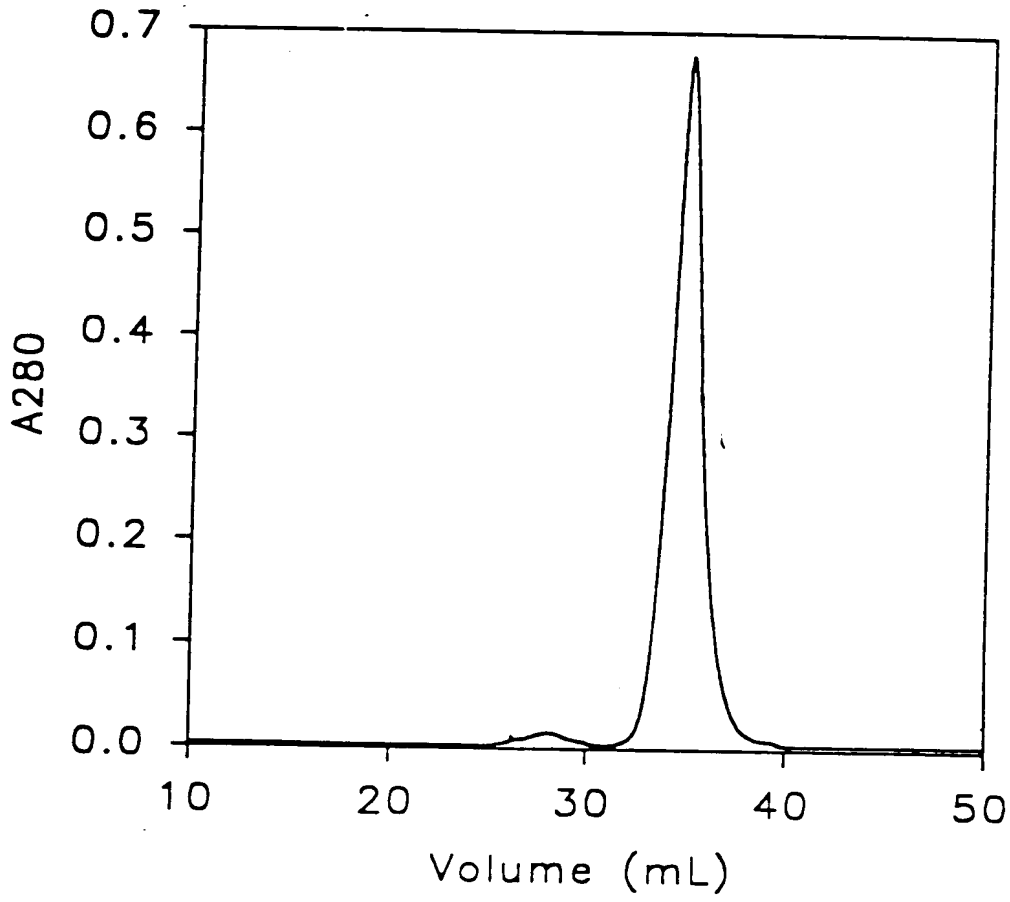
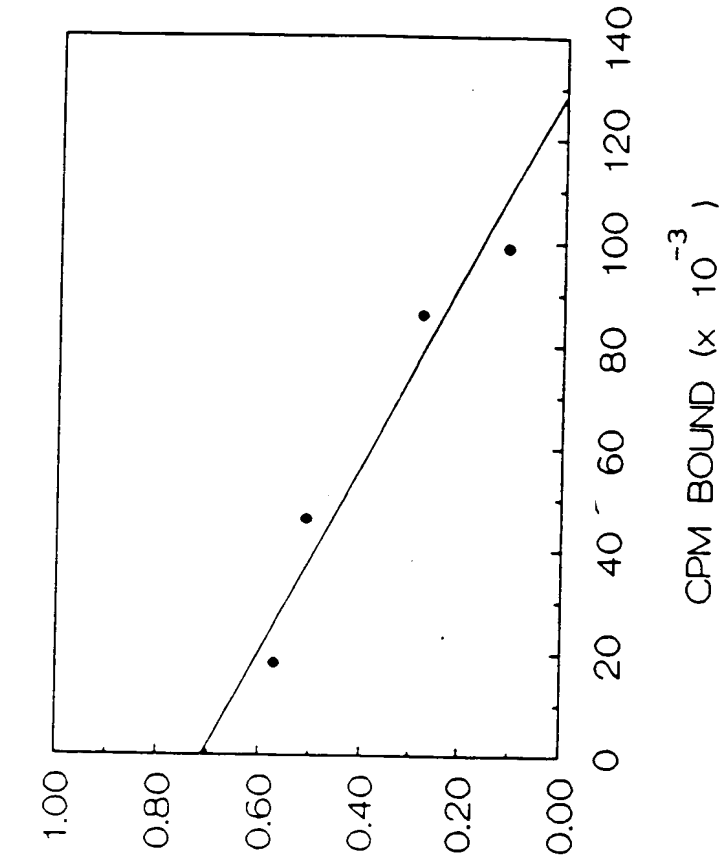


FIG. 41



B/F (Bound/Free^{125} I-SCF)

FIG. 42A

```
CCGCCTCGCGCCGAGACTAGAAGCGCTGCGGGAAGCAGGGACAGTGGAGAGGGCGCTGCGC   61

TCGGGCTACCCAATGCGTGGACTATCTGCCGCCGCTGTTCGTGCAATATGCTGGAGCTCCA  122

GAACAGCTAAACGGAGTCGCCACACCACTGTTTGTGCTGGATCGCAGCGCTGCCTTTCCTT  183

-25                 -20
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG    228

-10                                     1
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG    273

                10                                      20
Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA    318

                                        30
Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG    363

                40                                      50
Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA    408

                                        60
Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT    453
```

FIG. 42B

```
                    70                                                  80
Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val
ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG    498

                                   90
Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser
AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT    543

                  100                                       110
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT    588

                                  120
Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala
ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC    633

                  130                                       140
Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val
TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT    678

                                  150
Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg Val Ser Val Thr
TCT TCA ACA TTA AGT CCT GAG AAA GAT TCC AGA GTC AGT GTC ACA    723
```

FIG. 42C

```
                  160                                                 170
Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn
AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC AGC TCC CTT AGG AAT   768

                                      180
Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro Gly Asp
GAC AGC AGT AGC AGT AAT AGG AAG GCC AAA AAT CCC CCT GGA GAC   813

                  190                                         200
Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe Ser
TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG TTT TCT   858


                                      210
Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg
CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG AGA   903

                  220                                         230
Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu
CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA   948

                                  240
Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe
GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT   993

        248
Gln Glu Val End
CAA GAA GTG TAA      TTGTGGCTTGTATCAACACTGTTACTTTCGTACATTGGC 1044
```

FIG. 42D

TGGTAACAGTTCATGTTTGCTTCATAAATGAAGCAGCTTTAAACAAATTCATATTCTGTC 1104

TGGAGTGACAGACCACATCTTTATCTGTTCTTGCTACCCATGACTTTATATGGATGATTC 1164

AGAAATTGGAACAGAATGTTTTACTGTGAAACTGGCACTGAATTAATCATCTATAAAGAA 1224

GAACTTGCATGGAGCAGGACTCTATTTTAAGGACTGCGGGACTTGGGTCTCATTTAGAAC 1284

TTGCAGCTGATGTTGGAAGAGAAAGCACGTGTCTCAGACTGCATGTACCATTTGCATGGC 1344

TCCAGAAATGTCTAAATGCTGAAAAAACACCTAGCTTTATTCTTCAGATACAAACTGCAG 1404

FIG. 43

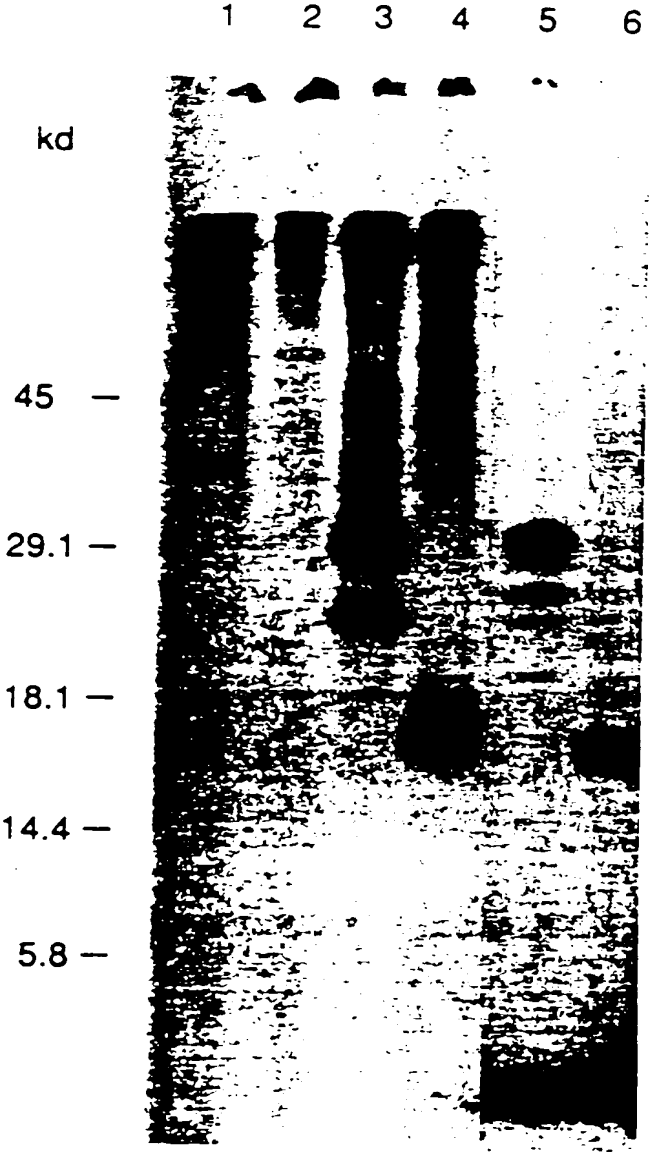


FIG. 44A

```
                                                AGCAGGGACAGTGGAGAGGGCGCTGCGCTC    30

GGGCTACCCAATGCGTGGACTATCTGCCGCCGCTGTTCGTGCAATATGCTGGAGCTCCAG    90

AACAGCTAAACGGAGTCGCCACACCACTGTTTGTGCTGGATCGCAGCGCTGCCTTTCCTT   150

-25                 -20
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG    195


-10                                             1
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG    240

                10                                          20
Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA    285

                                        30
Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG    330

                40                                          50
Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA    375
```

FIG. 44B

```
                                                  60
Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT   420

                  70                                      80
Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val
ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG   465

                                                  90
Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser
AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT   510

                 100                                     110
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT   555

                                                 120
Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala
ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC   600

                 130                                     140
Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val
TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT   645

                                                 150
Ser Ser Thr Leu Ser Pro Glu Lys | Gly | Lys Ala Lys Asn Pro Pro
TCT TCA ACA TTA AGT CCT GAG AAA | GGG | AAG GCC AAA AAT CCC CCT   690
```

FIG. 44C

```
                    160                                         170
Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu
GGA GAC TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG    735

                                        180
Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys
TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG    780

                    190                                         200
Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile
AAG AGA CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT    825

                                        210
Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg
AAT GAA GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA    870

                    220
Glu Phe Gln Glu Val End
GAG TTT CAA GAA GTG TAA     TTGTGGCTTGTATCAACACTGTTACTTTCGTA   920

CATTGGCTGGTAACAGTTCATGTTTGCTTCATAAATGAAGCAGCTTTAAACAAATTCATA   980

TTCTGTCTGGAGTGACAGACCACATCTTTATCTGTTCTTGCTACCCATGACTTTATATGG  1040

ATGATTCAGAAATTGGAACAGAATGTTTTACTGTGAAACTGGCACTGA              1088
```

FIG. 45

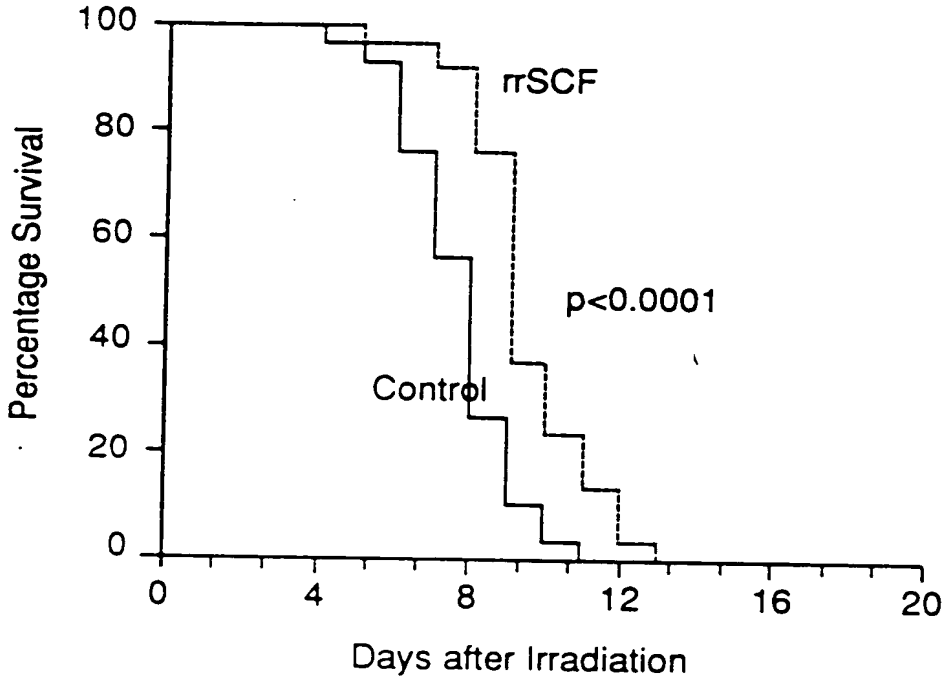
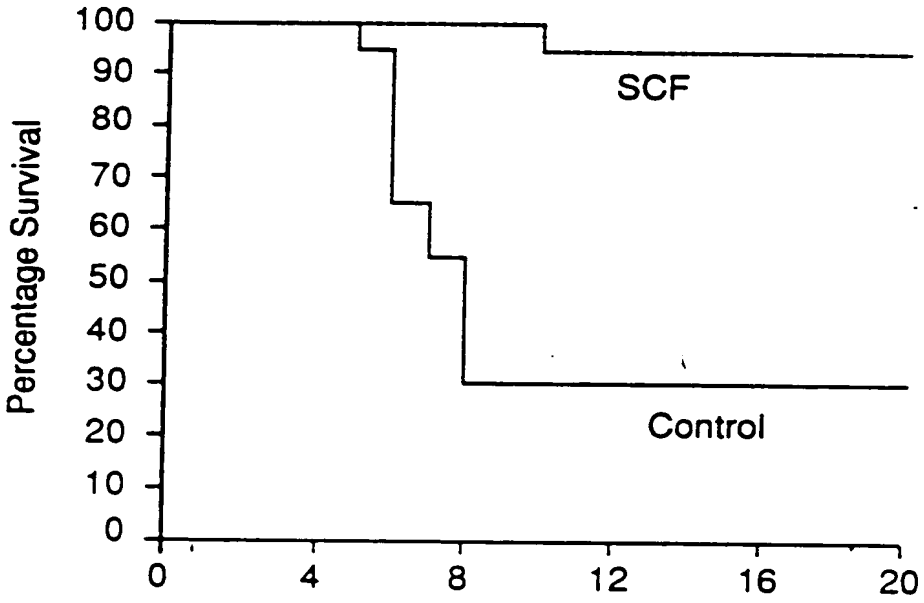

100
80
60
40
20
0
Percentage Survival
rrSCF
p<0.0001
Control
0
4
8
12
16
20
Days after Irradiation

FIG. 46



850 RADS; 5% of femur transplanted

FIG. 47

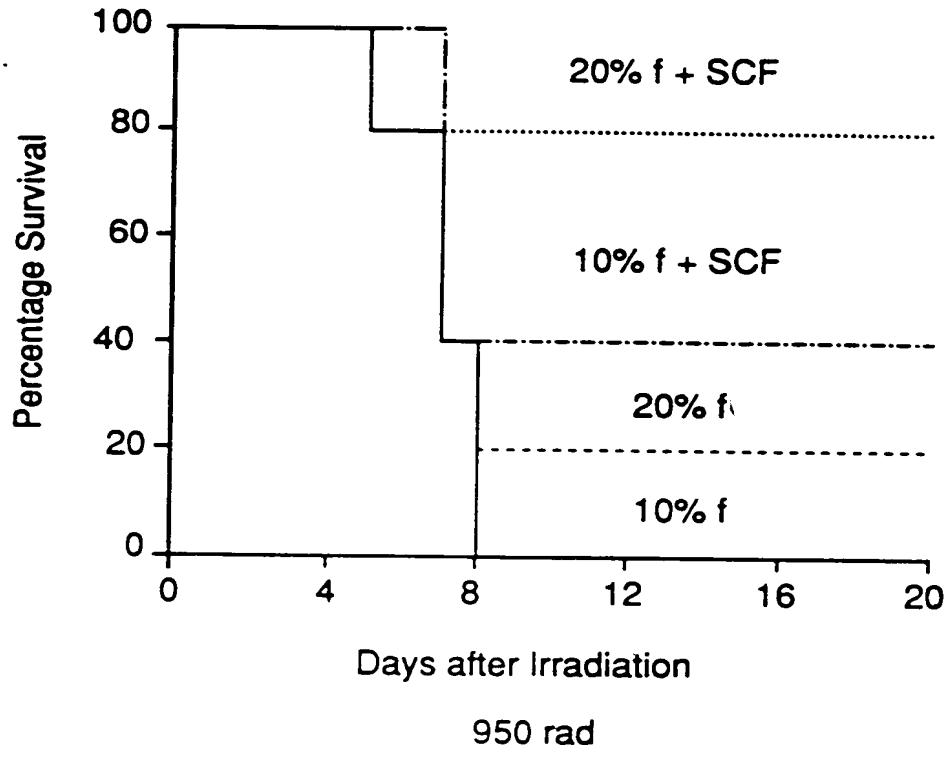

100
80
60
40
20
0
Percentage Survival
20% f + SCF
10% f + SCF
20% f
10% f
0
4
8
12
16
20
Days after Irradiation
950 rad

FIG. 48

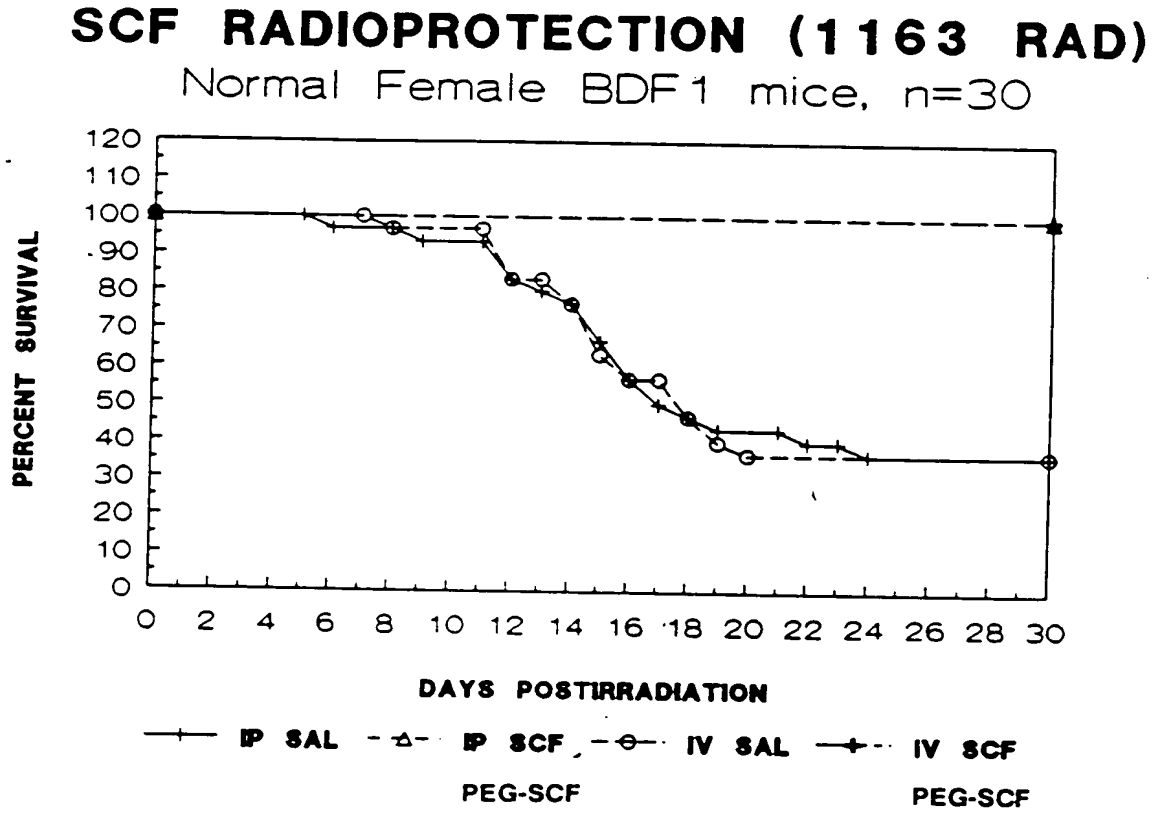

SCF RADIOPROTECTION (1163 RAD)
Normal Female BDF1 mice, n=30
PERCENT SURVIVAL
120
110
100
90
80
70
60
50
40
30
20
10
0
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30
DAYS POSTIRRADIATION
IP SAL
IP SCF
PEG-SCF
IV SAL
IV SCF
PEG-SCF

FIG. 49

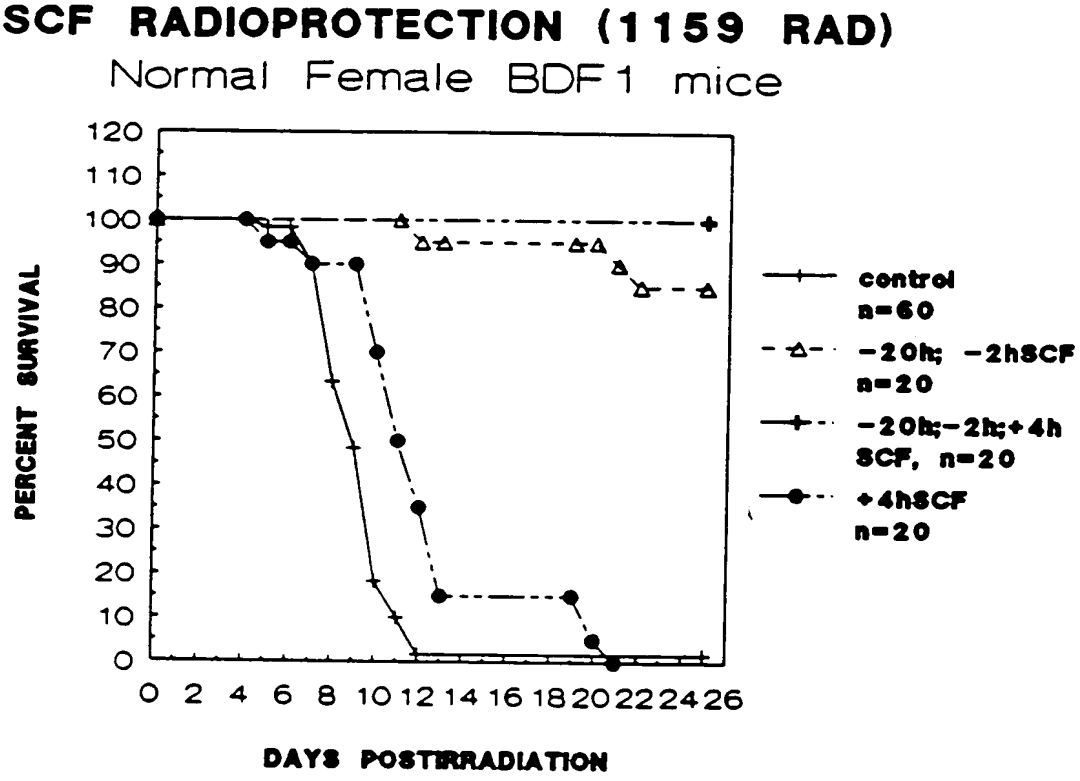

SCF RADIOPROTECTION (1159 RAD)
Normal Female BDF1 mice
PERCENT SURVIVAL
120
110
100
90
80
70
60
50
40
30
20
10
0
0 2 4 6 8 10 12 14 16 18 20 22 24 26
DAYS POSTIRRADIATION
control n=60
-20h; -2hSCF n=20
-20h;-2h;+4h SCF, n=20
+4hSCF n=20

FIG. 50

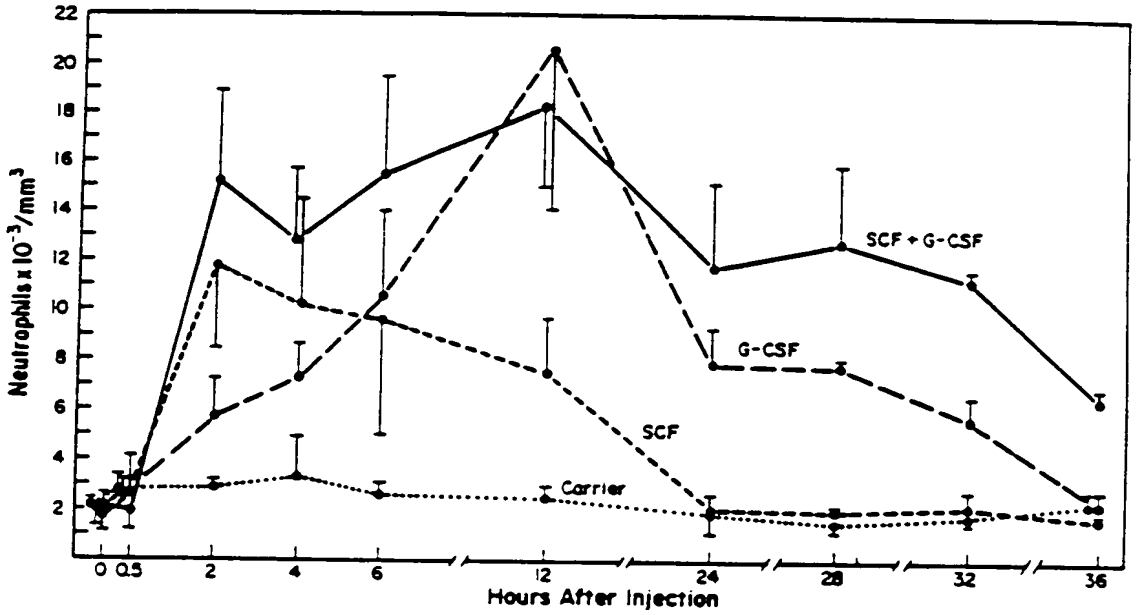

Neutrophils x 10^{-3}/mm^3
22
20
18
16
14
12
10
8
6
4
2
0
0.5
2
4
6
12
24
28
32
36
Hours After Injection
SCF + G-CSF
G-CSF
SCF
Carrier

FIG. 51

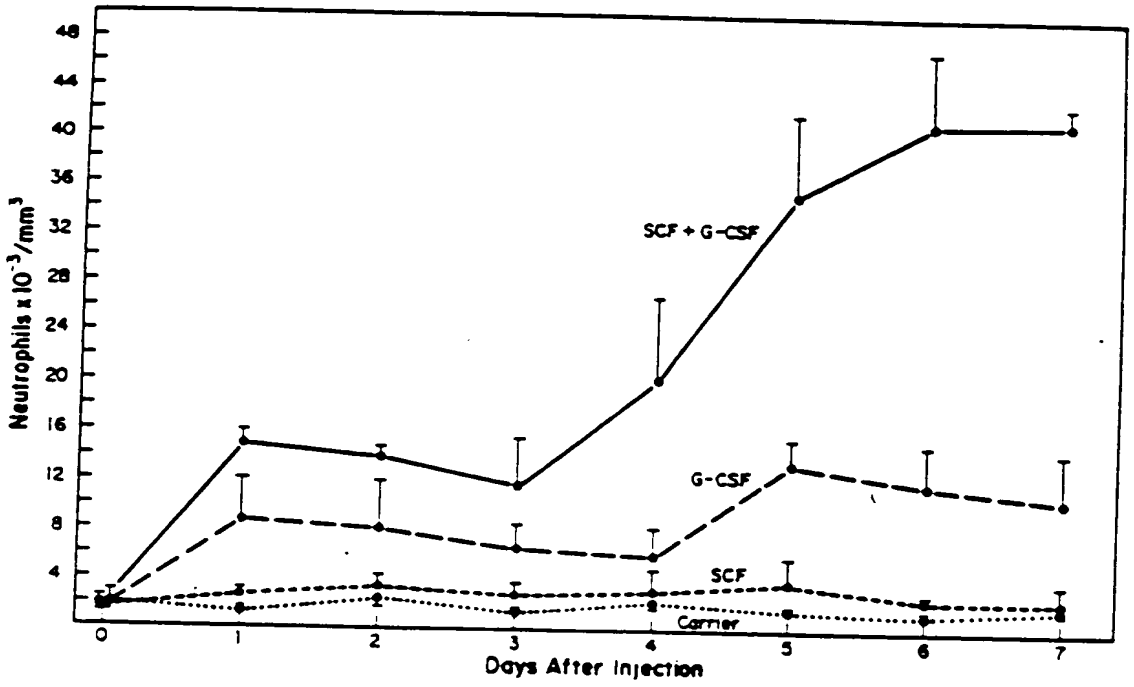

Neutrophils x 10^{-3}/mm^3
48
44
40
36
32
28
24
20
16
12
8
4
SCF + G-CSF
G-CSF
SCF
Carrier
0
1
2
3
4
5
6
7
Days After Injection

FIG. 52

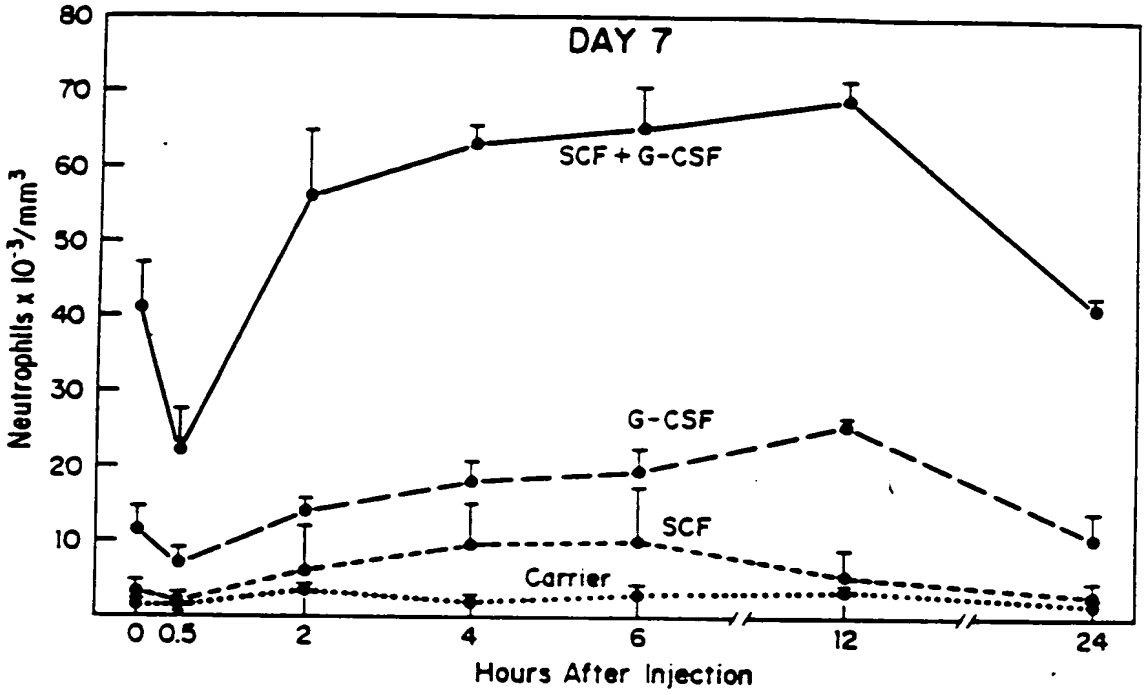

DAY 7
SCF + G-CSF
G-CSF
SCF
Carrier
Neutrophils x 10^{-3}/mm^3
80
70
60
50
40
30
20
10
0
0.5
2
4
6
12
24
Hours After Injection

FIG. 53

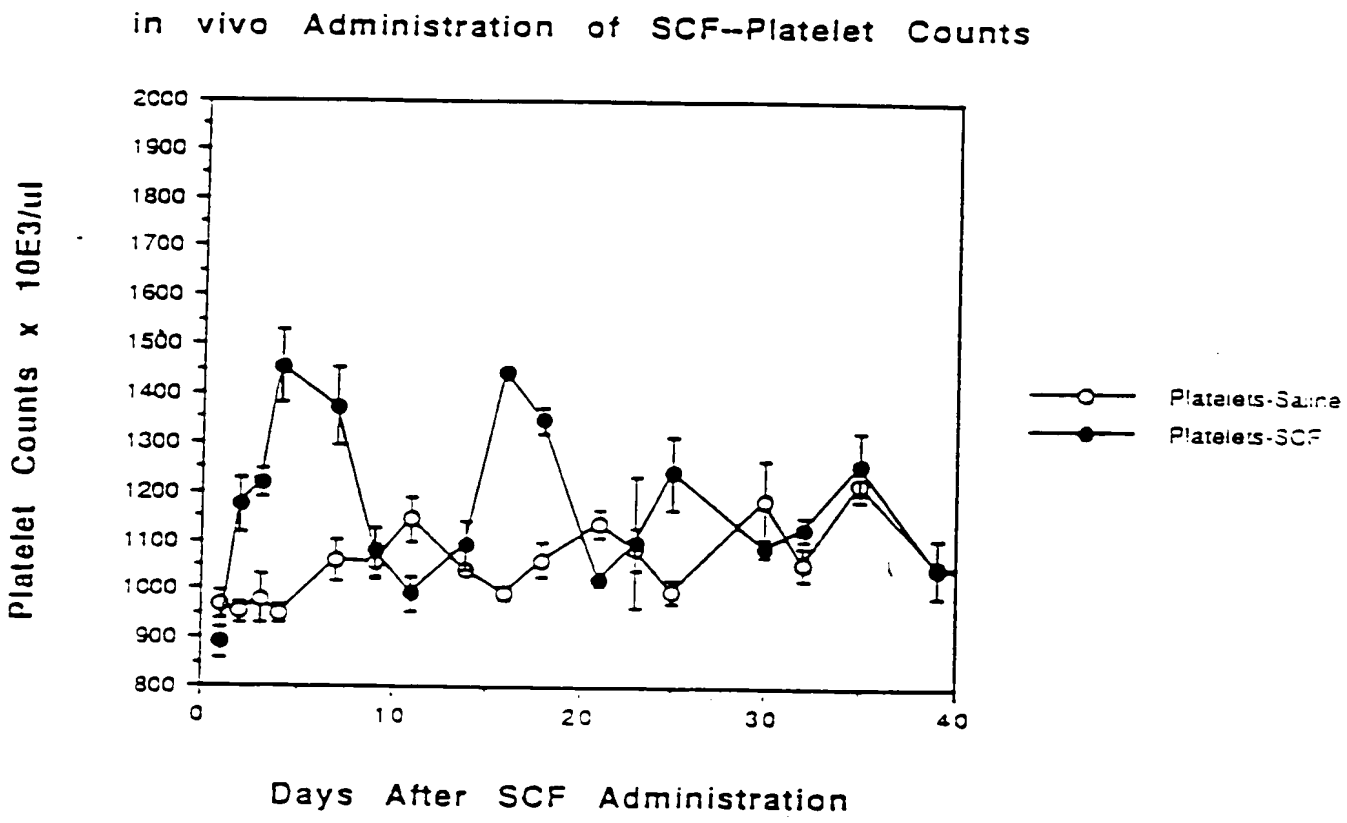

in vivo Administration of SCF--Platelet Counts
Platelet Counts x 10E3/ul
2000
1900
1800
1700
1600
1500
1400
1300
1200
1100
1000
900
800
0
10
20
30
40
Days After SCF Administration
Platelets-Saline
Platelets-SCF

FIG. 54

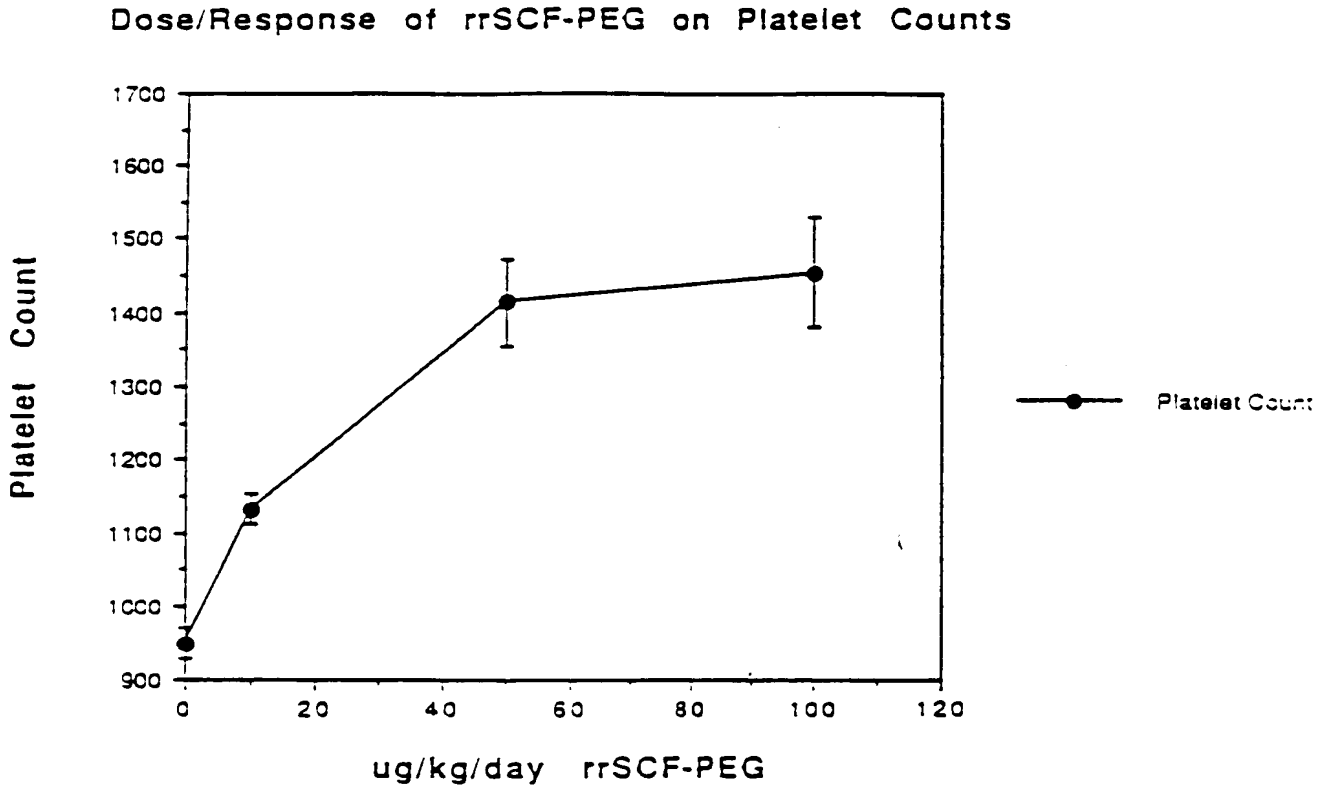

Dose/Response of rrSCF-PEG on Platelet Counts
Platelet Count
1700
1600
1500
1400
1300
1200
1100
1000
900
0
20
40
60
80
100
120
ug/kg/day rrSCF-PEG
Platelet Count

FIG. 55

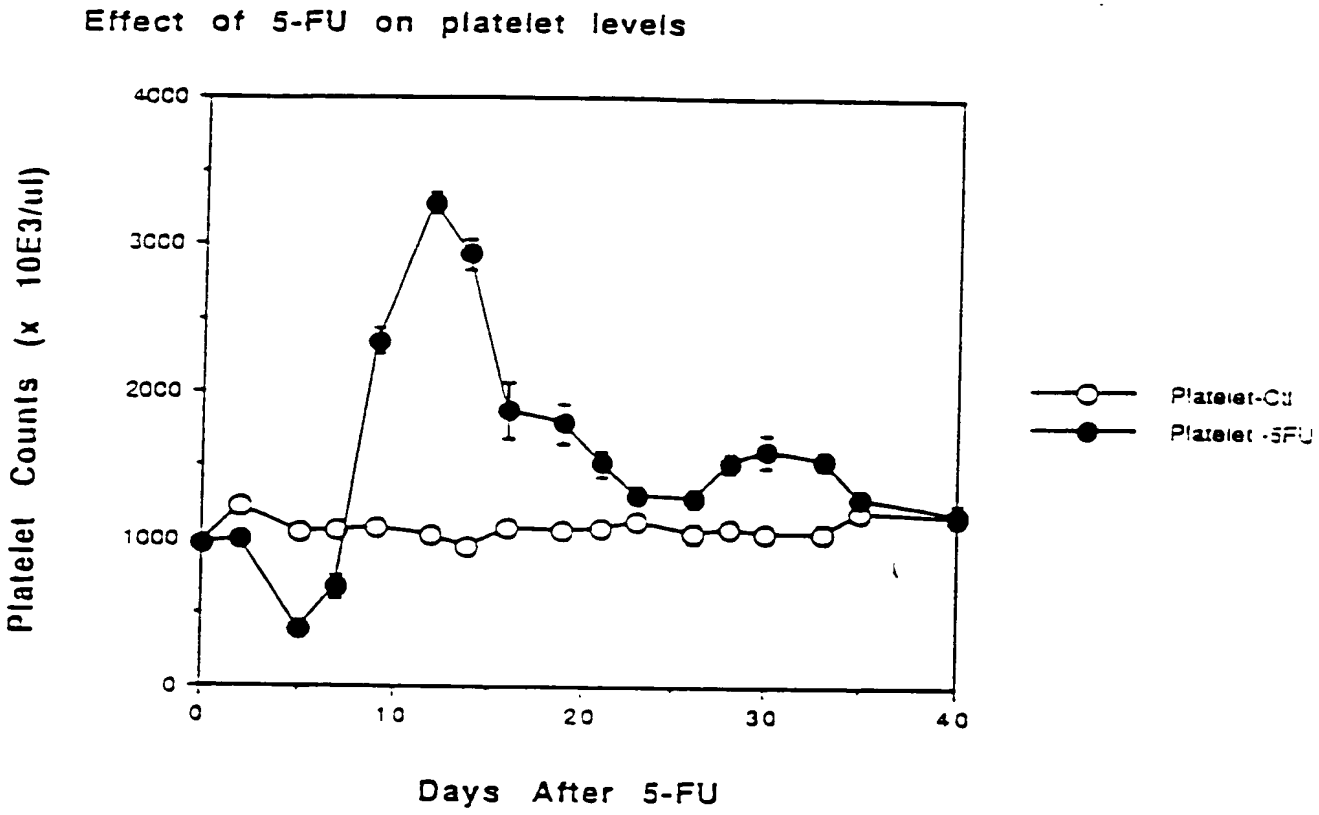

Effect of 5-FU on platelet levels
Platelet Counts (x 10E3/ul)
4000
3000
2000
1000
0
0
10
20
30
40
Days After 5-FU
Platelet-Cu
Platelet -5FU

FIG. 56

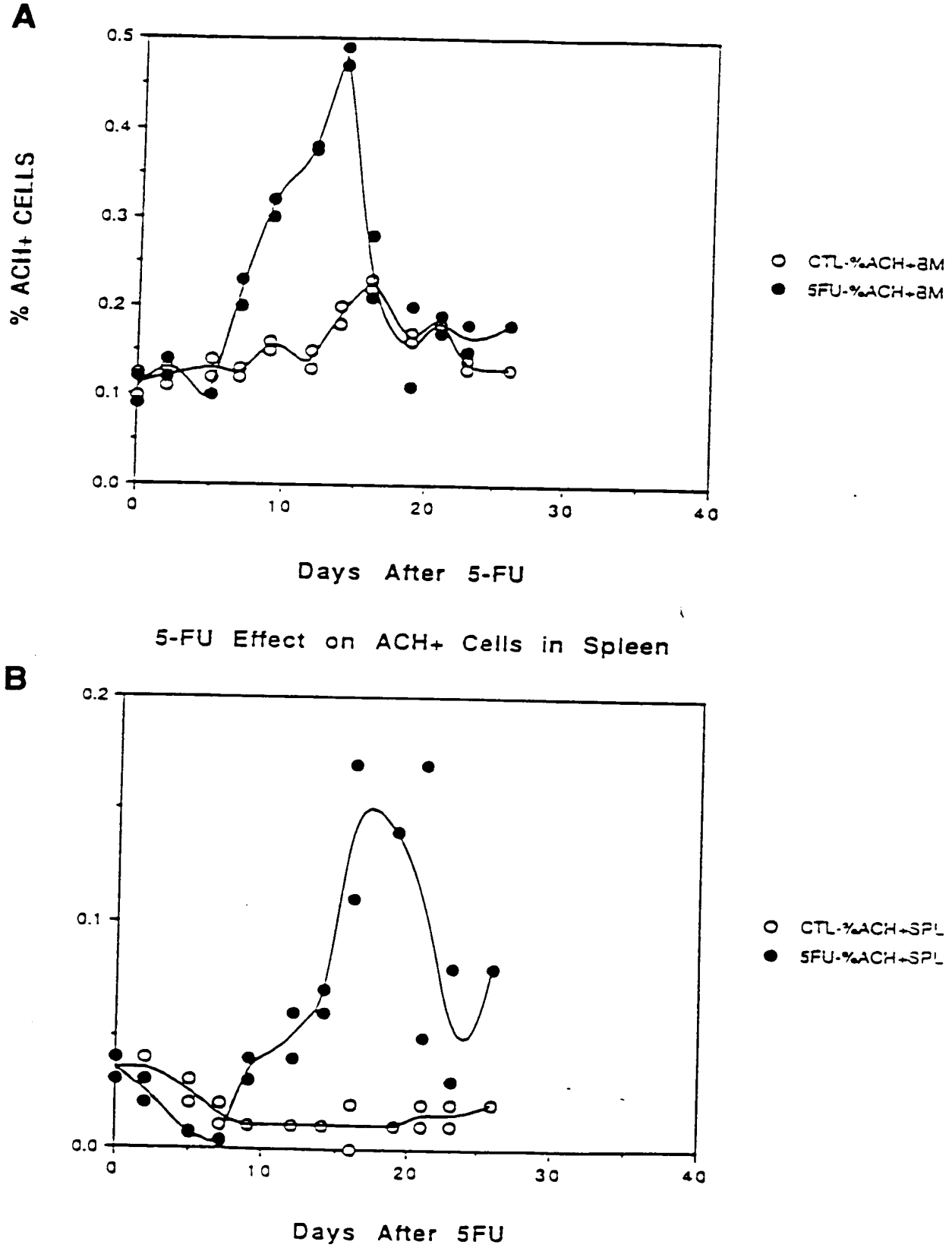

5-FU Effect on ACH+ Cells in Marrow
A
% ACH+ CELLS
0.5
0.4
0.3
0.2
0.1
0.0
0
10
20
30
40
Days After 5-FU
CTL-%ACH+BM
5FU-%ACH+BM
5-FU Effect on ACH+ Cells in Spleen
B
% ACH+ Cells
0.2
0.1
0.0
0
10
20
30
40
Days After 5FU
CTL-%ACH+SPL
5FU-%ACH+SPL

FIG. 57

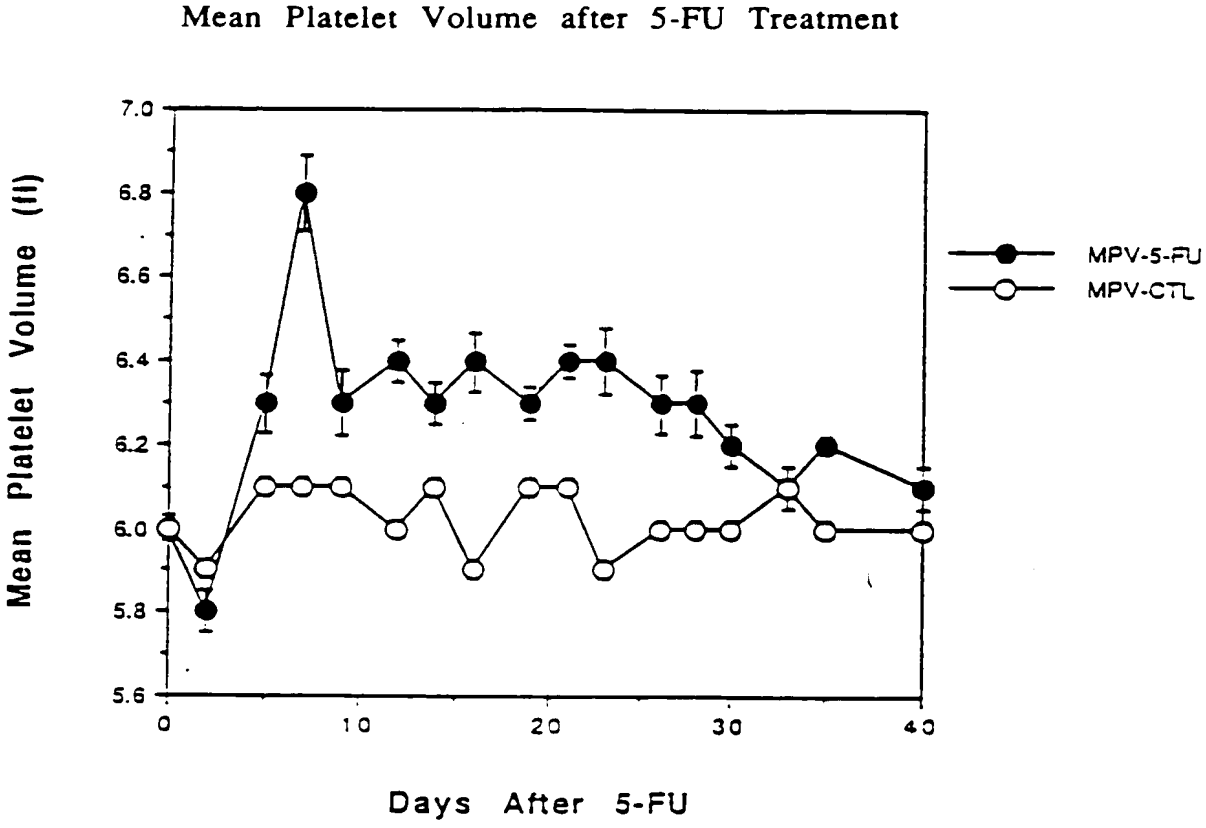

Mean Platelet Volume after 5-FU Treatment
Mean Platelet Volume (fl)
7.0
6.8
6.6
6.4
6.2
6.0
5.8
5.6
0
10
20
30
40
Days After 5-FU
MPV-5-FU
MPV-CTL

FIG. 58

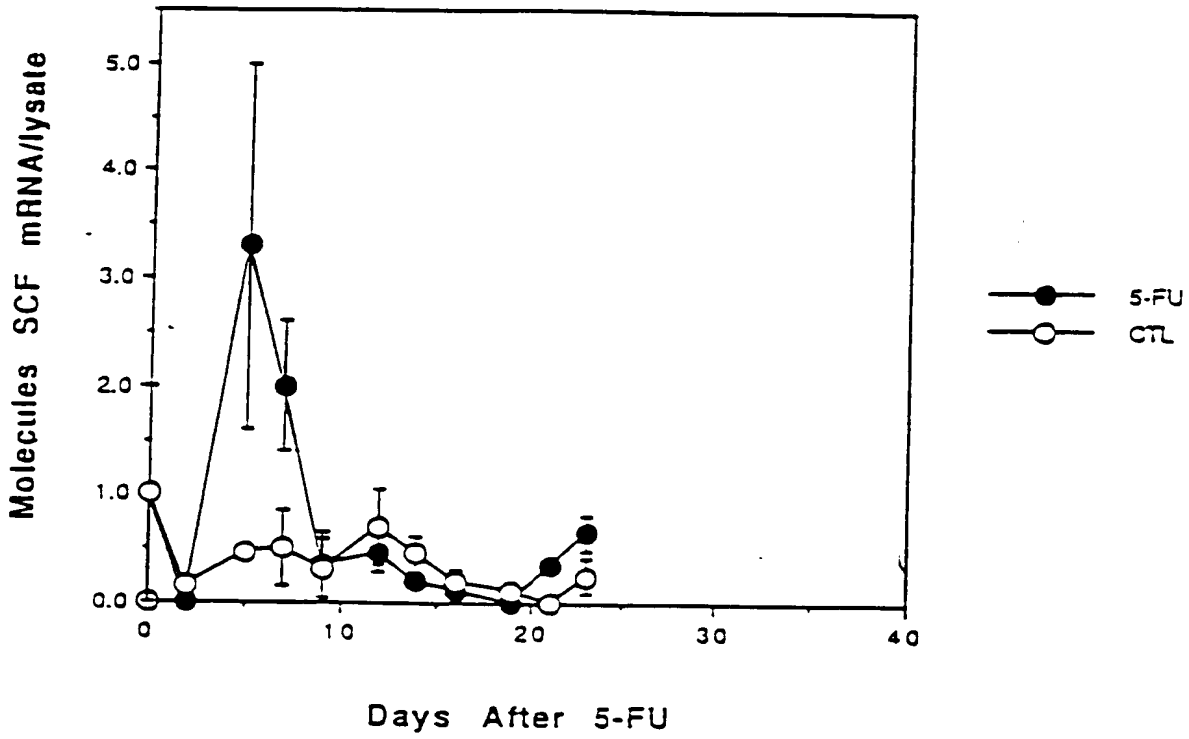

Molecules SCF mRNA/lysate
5.0
4.0
3.0
2.0
1.0
0.0
0
10
20
30
40
Days After 5-FU
5-FU
CTL

FIG. 59

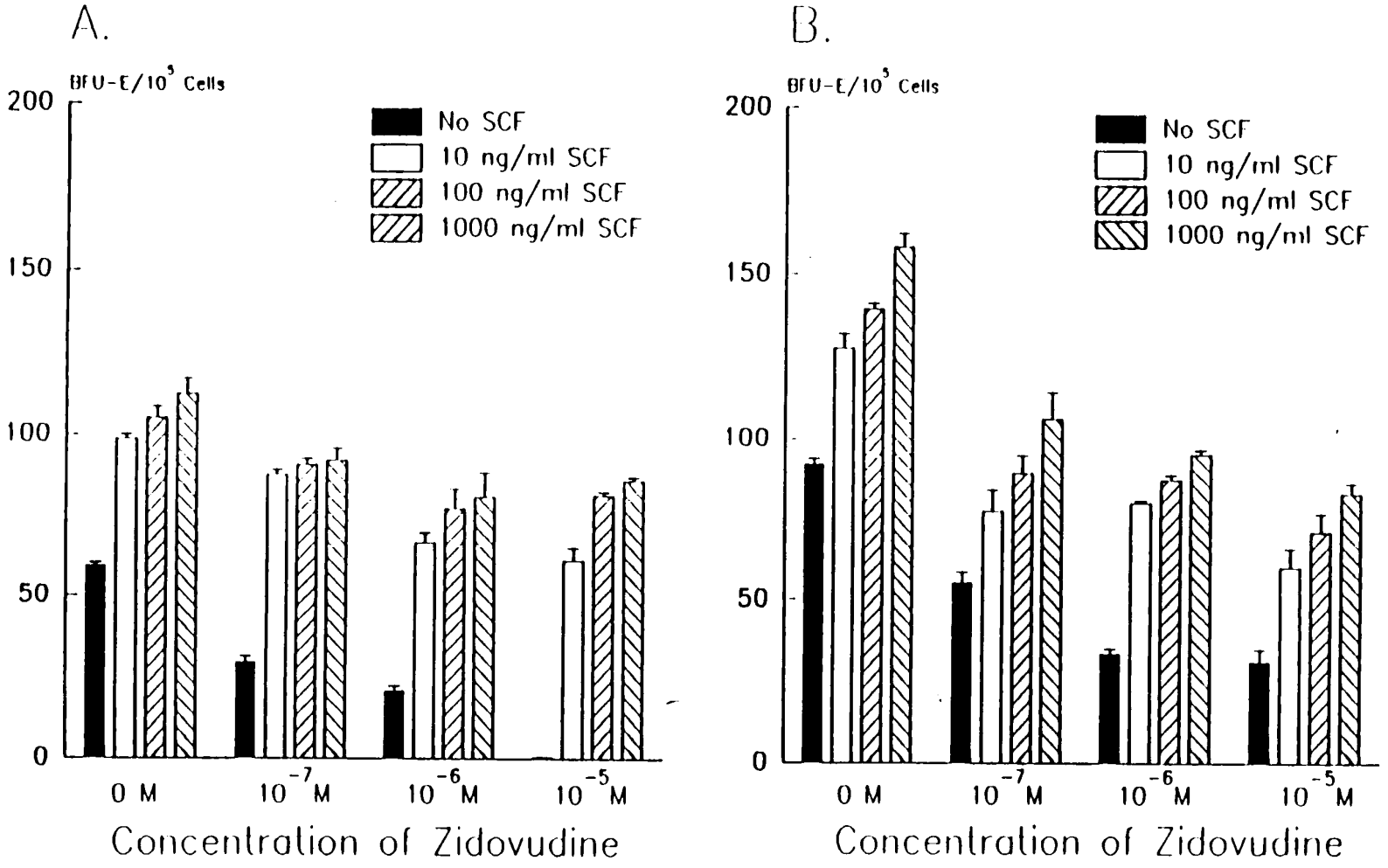

A.
BFU-E/10^5 Cells
200
150
100
50
0
No SCF
10 ng/ml SCF
100 ng/ml SCF
1000 ng/ml SCF
0 M
10^-7 M
10^-6 M
10^-5 M
Concentration of Zidovudine
B.
BFU-E/10^5 Cells
200
150
100
50
0
No SCF
10 ng/ml SCF
100 ng/ml SCF
1000 ng/ml SCF
0 M
10^-7 M
10^-6 M
10^-5 M
Concentration of Zidovudine

FIG. 60

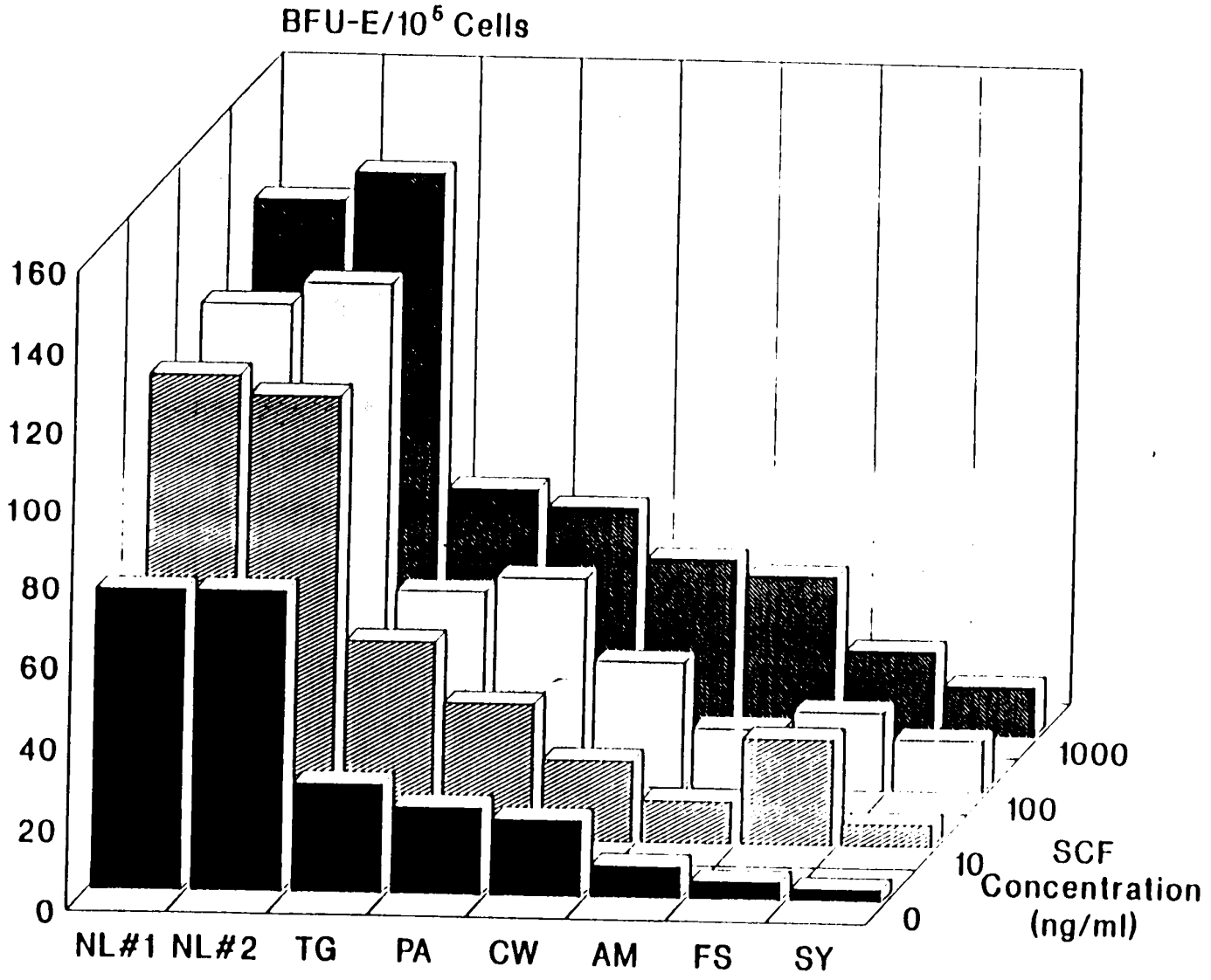

BFU-E/10^5 Cells
160
140
120
100
80
60
40
20
0
NL#1
NL#2
TG
PA
CW
AM
FS
SY
0
10
100
1000
SCF
Concentration
(ng/ml)

FIG: 61

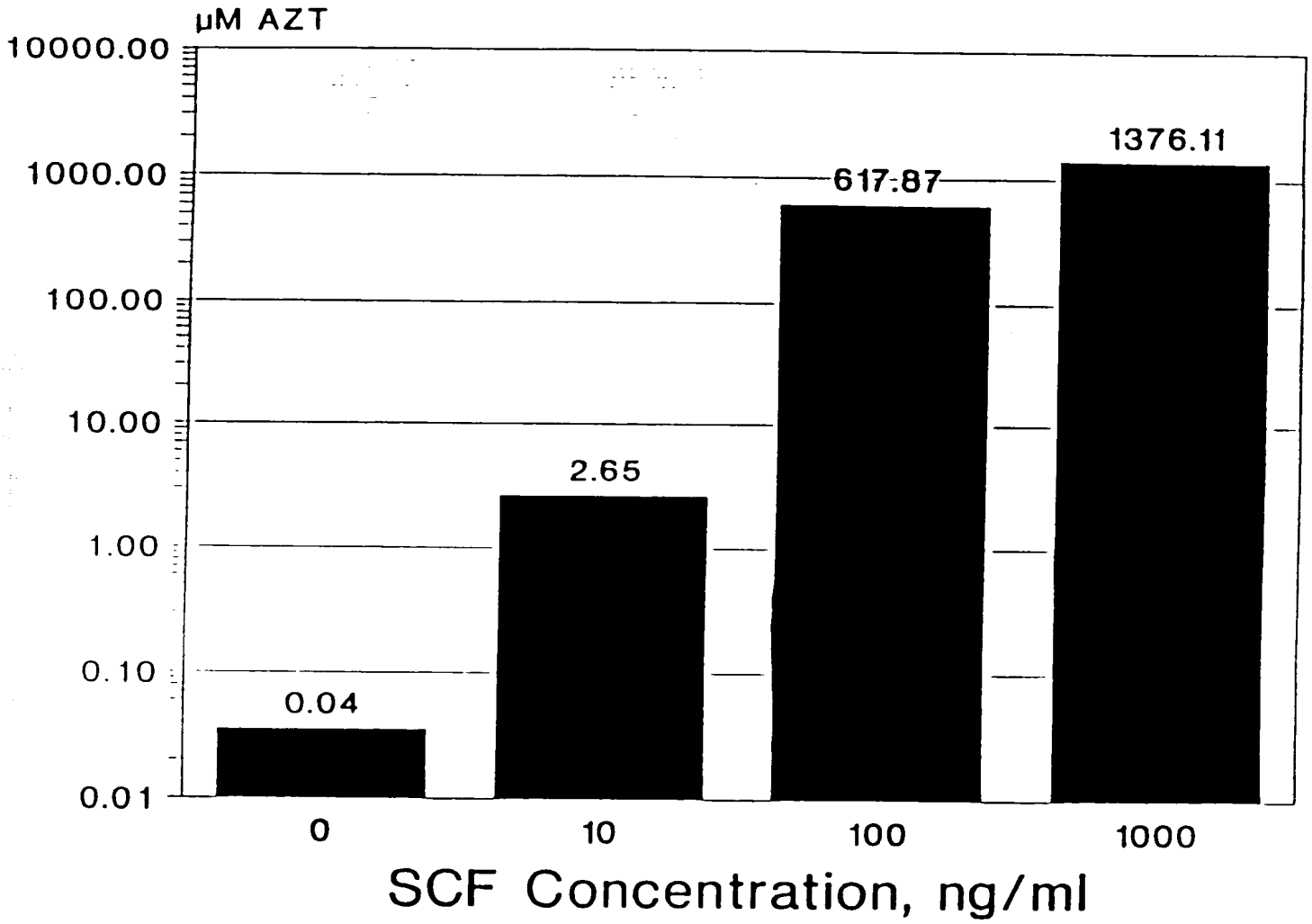

µM AZT
10000.00
1000.00
100.00
10.00
1.00
0.10
0.01
0.04
2.65
617.87
1376.11
0
10
100
1000
SCF Concentration, ng/ml

FIG. 62

EFFECT OF SCF ON AZT SUPPRESSION OF BMC

BFU-E

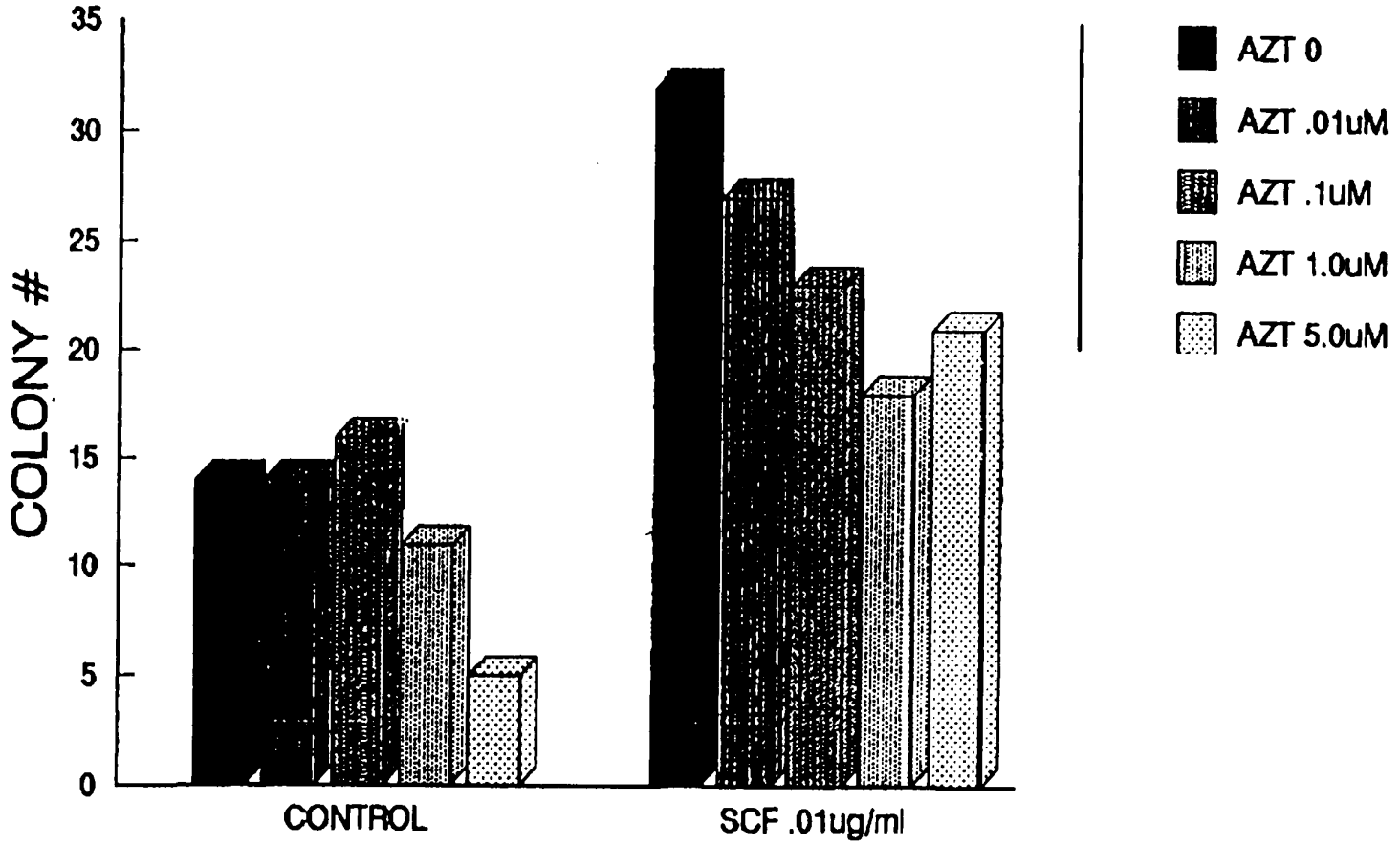


FIG. 63

EFFECT OF SCF ON AZT SUPPRESSION OF BMC

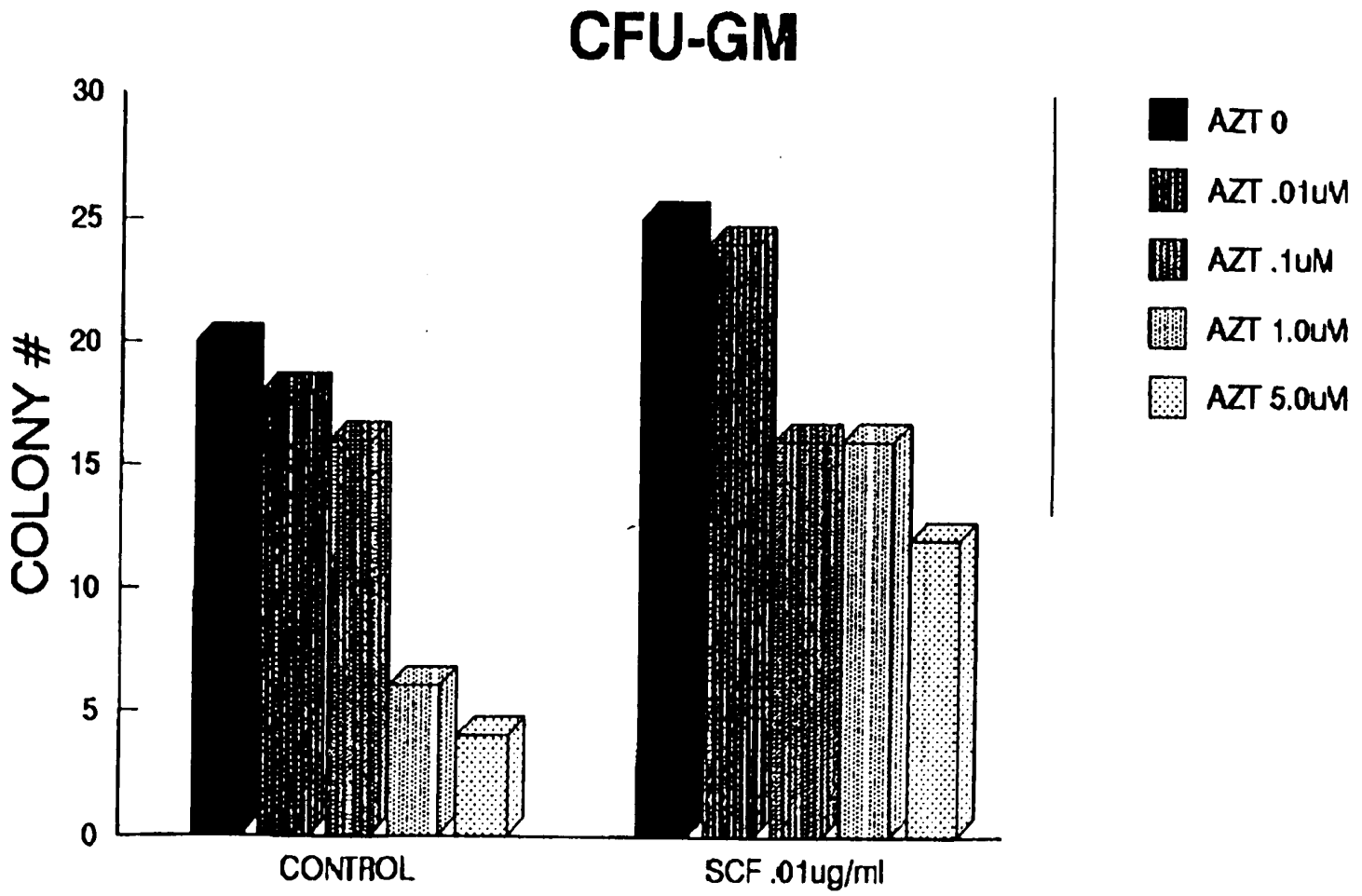


FIG. 64

EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC

BFU-E

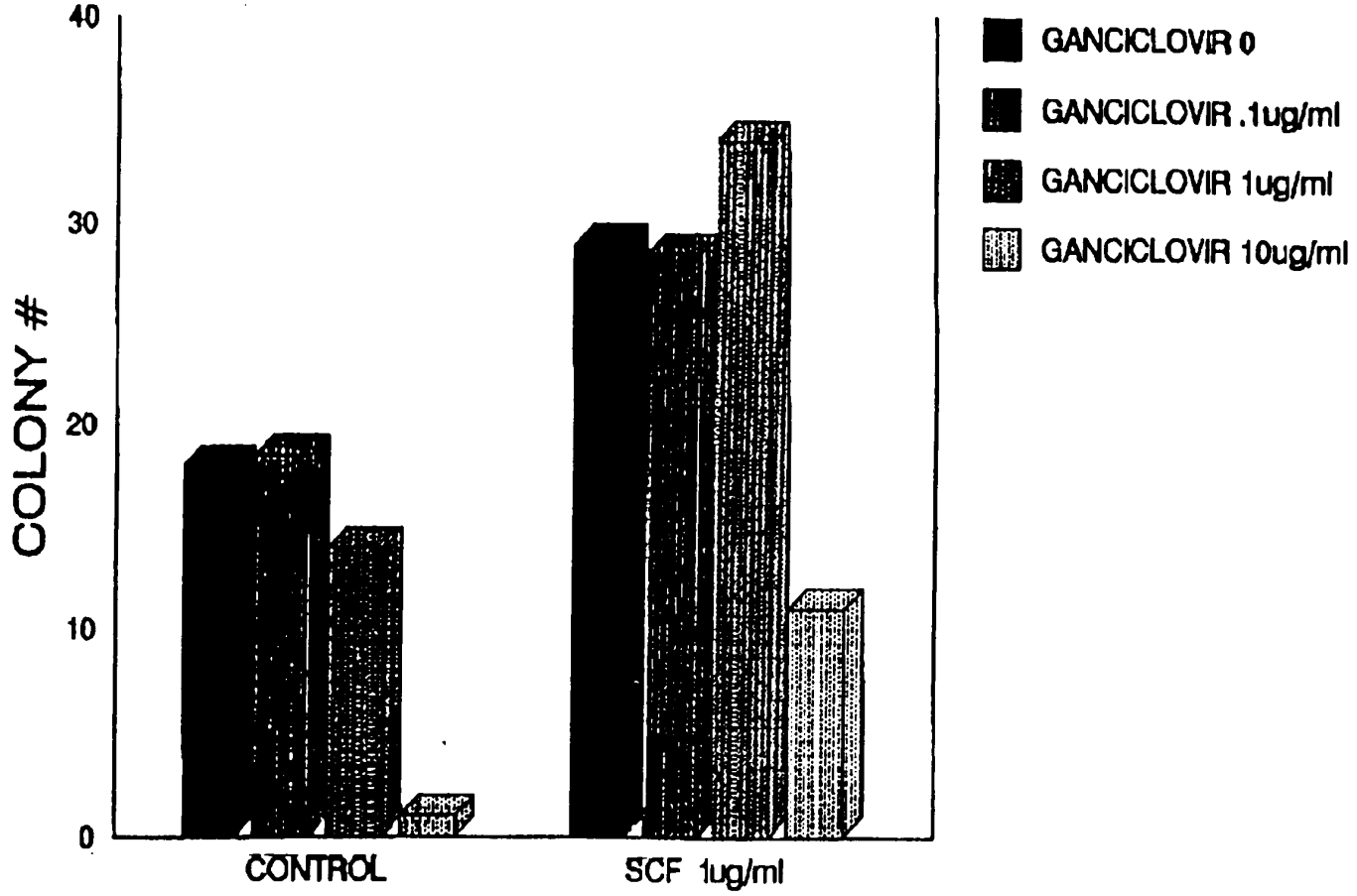


FIG. 65

EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC

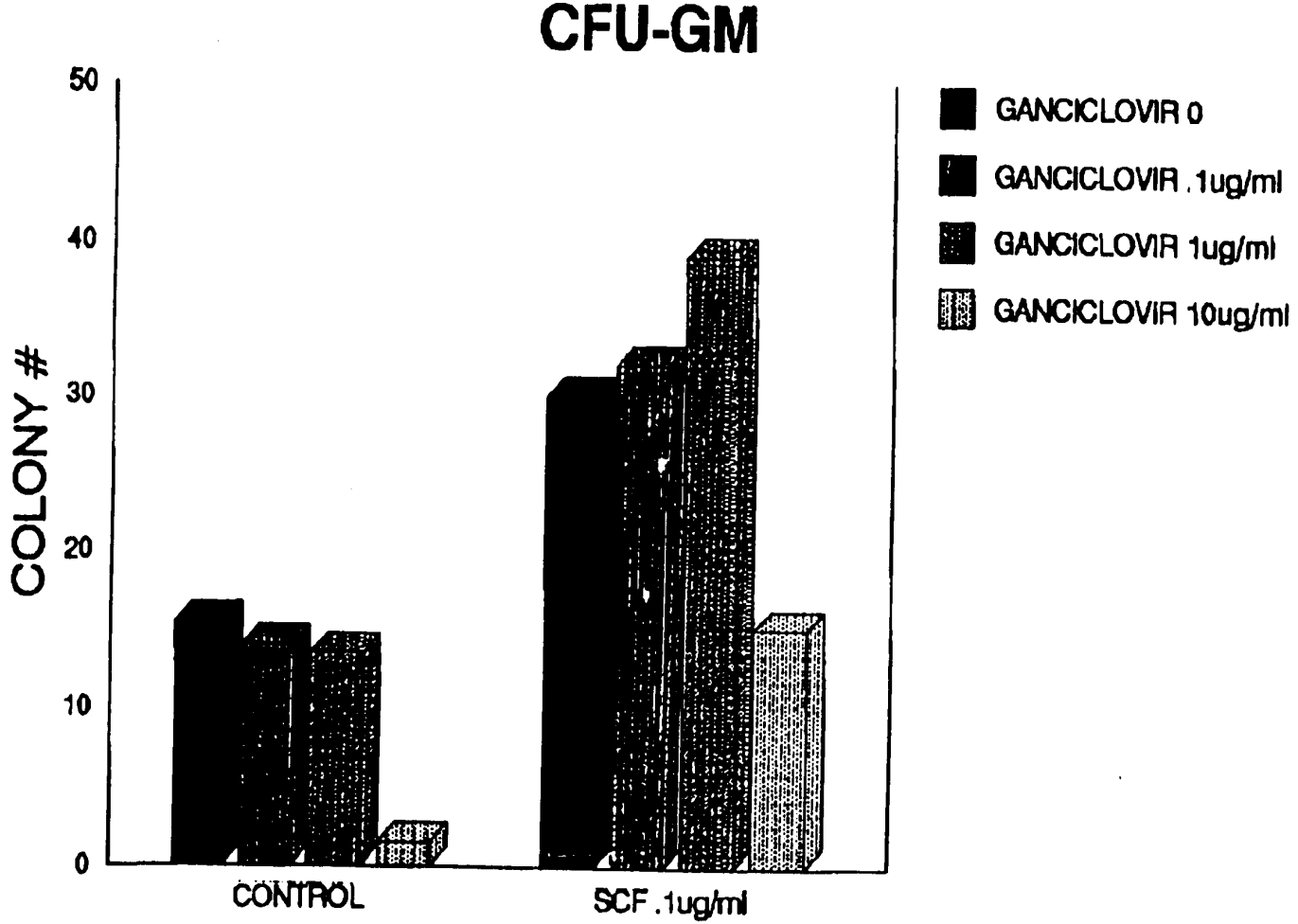


FIG. 66

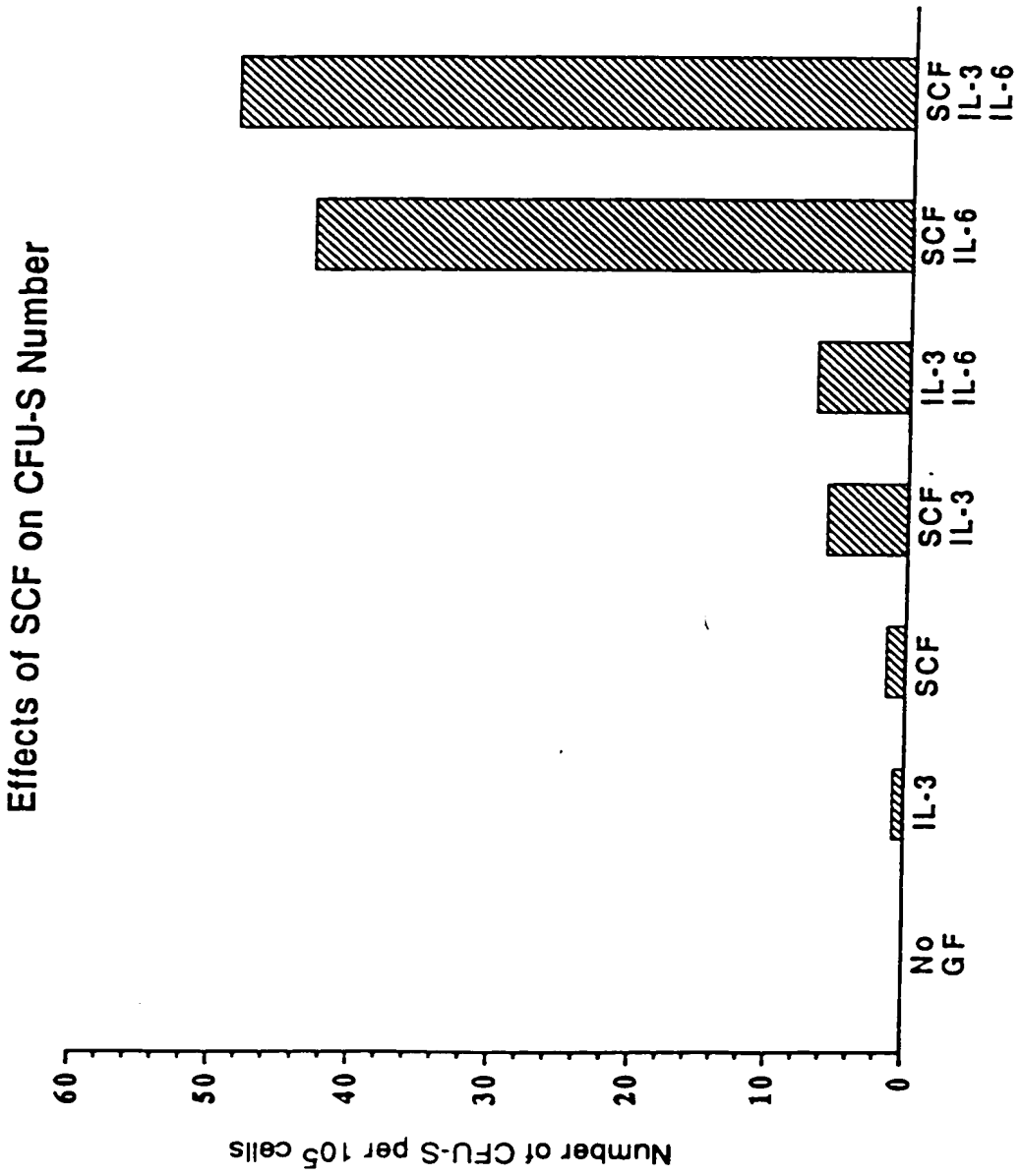

Effects of SCF on CFU-S Number
Number of CFU-S per 10^5 cells
0
10
20
30
40
50
60
No GF
IL-3
SCF
SCF IL-3
IL-3 IL-6
SCF IL-6
SCF IL-3 IL-6

FIG. 67

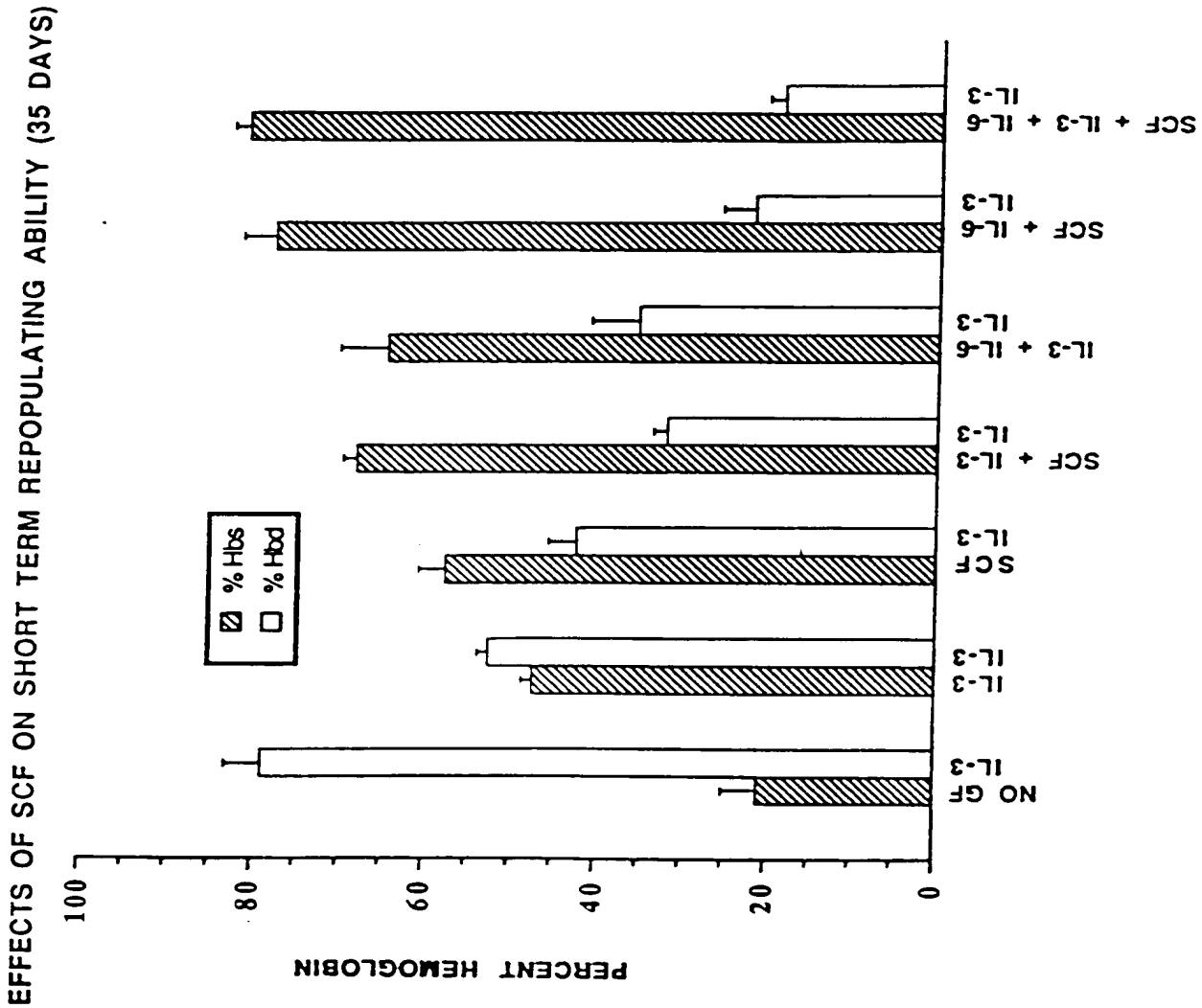

EFFECTS OF SCF ON SHORT TERM REPOPULATING ABILITY (35 DAYS)
PERCENT HEMOGLOBIN
0
20
40
60
80
100
% Hbs
% Hbd
NO GF
IL-3
IL-3
IL-3
SCF
IL-3
SCF + IL-3
IL-3
IL-3 + IL-6
IL-3
SCF + IL-6
IL-3
SCF + IL-3 + IL-6
IL-3

FIG. 68

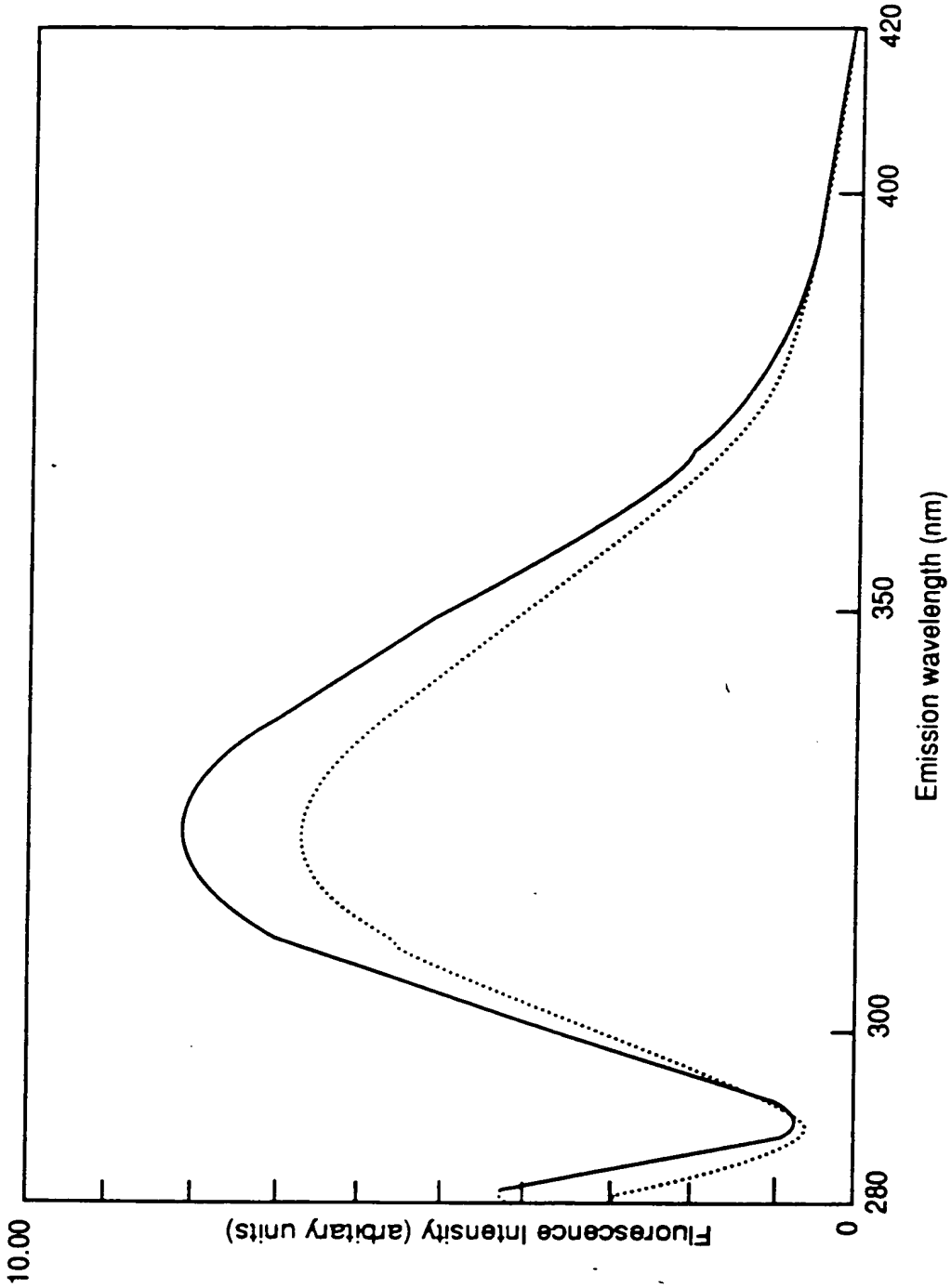

10.00
0
Fluorescence Intensity (arbitary units)
280
300
350
400
420
Emission wavelength (nm)

FIG. 69A

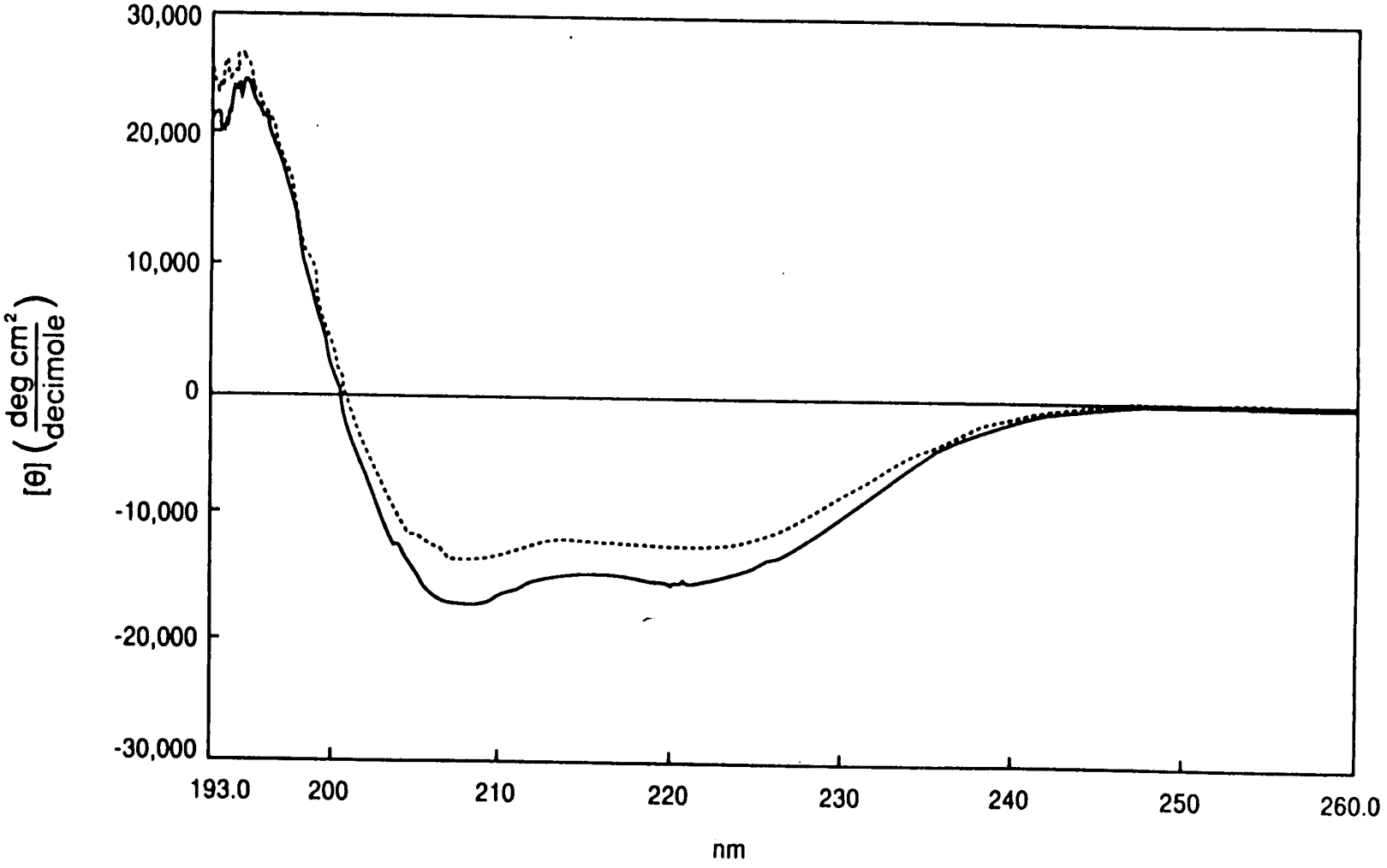

30,000
20,000
10,000
0
-10,000
-20,000
-30,000
[θ] (deg cm²/decimole)
193.0
200
210
220
230
240
250
260.0
nm

FIG. 69B

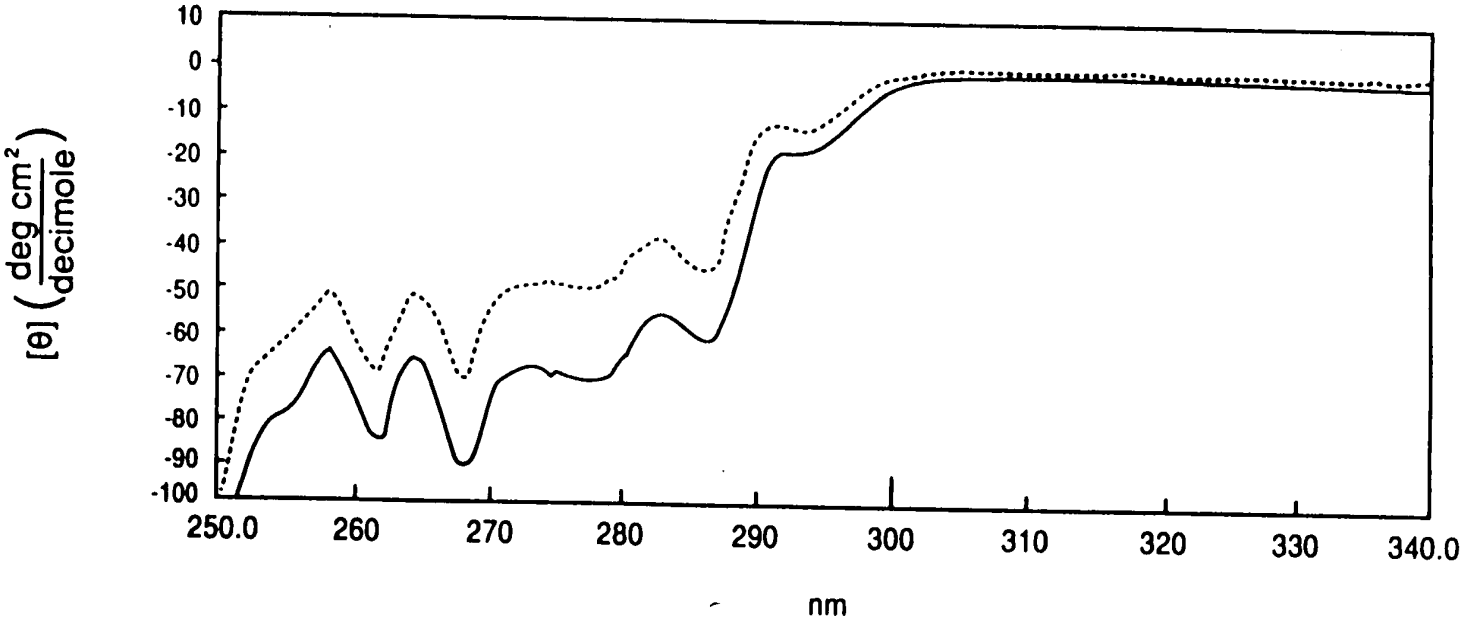

10
0
-10
-20
-30
-40
-50
-60
-70
-80
-90
-100
[θ] (deg cm²/decimole)
250.0
260
270
280
290
300
310
320
330
340.0
nm

FIG. 70

